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(54) Title: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES AND THEIR USE AS THERAPEUTIC AND DIAGNOSTIC AGENTS		
(57) Abstract The present invention relates to a polynucleic acid composition comprising or consisting of at least one polynucleic acid containing 8 or more contiguous nucleotides corresponding to a nucleotide sequence from the region spanning positions 417 to 957 of the Core/E1 region of HCV type 3; and/or the region spanning positions 4664 to 4730 of the NS3 region of HCV type 3; and/or the region spanning positions 4892 to 5292 of the NS3/4 region of HCV type 3; and/or the region spanning positions 8 023 to 8 235 of the NS5 region of the BR36 subgroup of HCV type 3a; and/or the coding region of HCV type 4a starting at nucleotide 379 in the core region; and/or the coding region of HCV type 4; and/or the coding region of HCV type 5, with said nucleotide numbering being with respect to the numbering of HCV nucleic acids as shown in Table 1, and with said polynucleic acids containing at least one nucleotide difference with known HCV type 1, and/or HCV type 2 genomes in the above-indicated regions, or the complement thereof.		

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NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES AND THEIR USE AS THERAPEUTIC AND DIAGNOSTIC AGENTS

The invention relates to new sequences of hepatitis C virus (HCV) genotypes and their use as therapeutic and diagnostic agents.

The present invention relates to new nucleotide and amino acid sequences corresponding to the coding region of a new type 2 subtype 2d, type-specific sequences corresponding to HCV type 3a, to new sequences corresponding to the coding region of a new subtype 3c, and to new sequences corresponding to the coding region of HCV type 4 and type 5 subtype 5a; a process for preparing them, and their use for diagnosis, prophylaxis and therapy.

The technical problem underlying the present invention is to provide new type-specific sequences of the Core, the E1, the E2, the NS3, the NS4 and the NS5 regions of HCV type 4 and type 5, as well as of new variants of HCV types 2 and 3. These new HCV sequences are useful to diagnose the presence of type 2 and/or type 3 and/or type 4 and/or type 5 HCV genotypes in a biological sample. Moreover, the availability of these new type-specific sequences can increase the overall sensitivity of HCV detection and should also prove to be useful for therapeutic purposes.

Hepatitis C viruses (HCV) have been found to be the major cause of non-A, non-B hepatitis. The sequences of cDNA clones covering the complete genome of several prototype isolates have been determined (Kato et al., 1990; Choo et al., 1991; Okamoto et al., 1991; Okamoto et al., 1992). Comparison of these isolates shows that the variability in nucleotide sequences can be used to distinguish at least 2 different genotypes, type 1 (HCV-1 and HCV-J) and type 2 (HC-J6 and HC-J8), with an average homology of about 68%. Within each type, at least two subtypes exist (e.g. represented by HCV-1 and HCV-J), having an average homology of about 79%. HCV genomes belonging to the same subtype show average homologies of more than 90% (Okamoto et al., 1992). However, the partial nucleotide sequence of the NS5 region of the HCV-T isolates showed at most 67% homology with the previously published sequences, indicating the existence of a yet another HCV type (Mori et al., 1992). Parts of the 5' untranslated region (UR), core, NS3, and NS5 regions of this type 3 have been published, further establishing the similar evolutionary distances between the 3 major genotypes and their subtypes (Chan et al., 1992).

The identification of type 3 genotypes in clinical samples can be achieved by means of PCR with type-specific primers for the NS5 region. However, the degree to which this will

be successful is largely dependent on sequence variability and on the virus titer present in the serum. Therefore, routine PCR in the open reading frame, especially for type 3 and the new type 4 and 5 described in the present invention and/or group V (Cha et al., 1992) genotypes can be predicted to be unsuccessful. A new typing system (LiPA), based on variation in the highly conserved 5' UR, proved to be more useful because the 5 major HCV genotypes and their subtypes can be determined (Stuyver et al., 1993). The selection of high-titer isolates enables to obtain PCR fragments for cloning with only 2 primers, while nested PCR requires that 4 primers match the unknown sequences of the new type 3, 4 and 5 genotypes.

New sequences of the 5' untranslated region (5'UR) have been listed by Bukh et al. (1992). For some of these, the E1 region has recently been described (Bukh et al., 1993). Isolates with similar sequences in the 5'UR to a group of isolates including DK12 and HK10 described by Bukh et al. (1992) and E-b1 to E-b8 described and classified as type 3 by Chan et al. (1991), have been reported and described in the 5'UR, the carboxyterminal part of E1, and in the NS5 region as group IV by Cha et al. (1992; WO 92/19743), and have also been described in the 5'UR for isolate BR56 and classified as type 3 by the inventors of this application (Stuyver et al., 1993).

The aim of the present invention is to provide new HCV nucleotide and amino acid sequences enabling the detection of HCV infection.

Another aim of the present invention is to provide new nucleotide and amino acid HCV sequences enabling the classification of infected biological fluids into different serological groups unambiguously linked to types and subtypes at the genome level.

Another aim of the present invention is to provide new nucleotide and amino acid HCV sequences ameliorating the overall HCV detection rate.

Another aim of the present invention is to provide new HCV sequences, useful for the design of HCV vaccine compositions.

Another aim of the present invention is to provide a pharmaceutical composition consisting of antibodies raised against the polypeptides encoded by these new HCV sequences, for therapy or diagnosis.

The present invention relates more particularly to a composition comprising or consisting of at least one polynucleic acid containing at least 5, and preferably 8 or more contiguous nucleotides selected from at least one of the following HCV sequences:

- an HCV type 3 genomic sequence, more particularly in any of the following regions:

- the region spanning positions 417 to 957 of the Core/E1 region of HCV subtype 3a,
- the region spanning positions 4664 to 4730 of the NS3 region of HCV type 3,
- the region spanning positions 4892 to 5292 of the NS3/4 region of HCV type 3,
- the region spanning positions 8023 to 8235 of the NS5 region of the BR36 subgroup of HCV subtype 3a,
- an HCV subtype 3c genomic sequence,

more particularly the coding regions of the above-specified regions;

- an HCV subtype 2d genomic sequence, more particularly the coding region of HCV subtype 2d;
- an HCV type 4 genomic sequence, more particularly the coding region, more particularly the coding region of subtypes 4a, 4e, 4f, 4g, 4h, 4i, and 4j,
- an HCV type 5 genomic sequence, more particularly the coding region of HCV type 5, more particularly the regions encoding Core, E1, E2, NS3, and NS4

with said nucleotide numbering being with respect to the numbering of HCV nucleic acids as shown in Table 1, and with said polynucleic acids containing at least one nucleotide difference with known HCV (type 1, type 2, and type 3) polynucleic acid sequences in the above-indicated regions, or the complement thereof.

It is to be noted that the nucleotide difference in the polynucleic acids of the invention may involve or not an amino acid difference in the corresponding amino acid sequences coded by said polynucleic acids.

According to a preferred embodiment, the present invention relates to a composition comprising or containing at least one polynucleic acid encoding an HCV polyprotein, with said polynucleic acid containing at least 5, preferably at least 8 nucleotides corresponding to at least part of an HCV nucleotide sequence encoding an HCV polyprotein, and with said HCV polyprotein containing in its sequence at least one of the following amino acid residues: L7, Q43, M44, S60, R67, Q70, T71, A79, A87, N106, K115, A127, A190, S130, V134, G142, I144, E152, A157, V158, P165, S177 or Y177, I178, V180 or E180 or F182, R184, I186, H187, T189, A190, S191 or G191, Q192 or L192 or I192 or V192 or E192, N193 or H193 or P193, W194 or Y194, H195, A197 or I197 or V197 or T197, V202, I203 or L203, Q208, A210, V212, F214, T216, R217 or D217 or E217 or V217, H218 or N218, H219 or

V219 or L219, L227 or I227, M231 or E231 or Q231, T232 or D232 or A232 or K232, Q235 or I235, A237 or T237, I242, I246, S247, S248, V249, S250 or Y250, I251 or V251 or M251 or F251, D252, T254 or V254, L255 or V255, E256 or A256, M258 or F258 or V258, A260 or Q260 or S260, A261, T264 or Y264, M265, I266 or A266, A267, G268 or T268, F271 or M271 or V271, I277, M280 or H280, I284 or A284 or L84, V274, V291, N292 or S292, R293 or I293 or Y293, Q294 or R294, L297 or I297 or Q297, A299 or K299 or Q299, N303 or T303, T308 or L308, T310 or F310 or A310 or D310 or V310, L313, G317 or Q317, L333, S351, A358, A359, A363, S364, A366, T369, L373, F376, Q386, I387, S392, I399, F402, I403, R405, D454, A461, A463, T464, K484, Q500, E501, S521, K522, H524, N528, S531, S532, V534, F536, F537, M539, I546, C1282, A1283, H1310, V1312, Q1321, P1368, V1372, V1373, K1405, Q1406, S1409, A1424, A1429, C1435, S1436, S1456, H1496, A1504, D1510, D1529, I1543, N1567, D1556, N1567, M1572, Q1579, L1581, S1583, F1585, V1595, E1606 or T1606, M1611, V1612 or L1612, P1630, C1636, P1651, T1656 or I1656, L1663, V1667, V1677, A1681, H1685, E1687, G1689, V1695, A1700, Q1704, Y1705, A1713, A1714 or S1714, M1718, D1719, A1721 or T1721, R1722, A1723 or V1723, H1726 or G1726, E1730, V1732, F1735, I1736, S1737, R1738, T1739, G1740, Q1741, K1742, Q1743, A1744, T1745, L1746, E1747 or K1747, I1749, A1750, T1751 or A1751, V1753, N1755, K1756, A1757, P1758, A1759, H1762, T1763, Y1764, P2645, A2647, K2650, K2653 or L2653, S2664, N2673, F2680, K2681, L2686, H2692, Q2695 or L2695 or I2695, V2712, F2715, V2719 or Q2719, T2722, T2724, S2725, R2726, G2729, Y2735, H2739, I2748, G2746 or I2746, I2748, P2752 or K2752, P2754 or T2754, T2757 or P2757, with said notation being composed of a letter representing the amino acid residue by its one-letter code, and a number representing the amino acid numbering according to Kato et al., 1990.

Each of the above-mentioned residues can be found in any of Figures 2, 5, 7, 11 or 12 showing the new amino acid sequences of the present invention aligned with known sequences of other types or subtypes of HCV for the Core, E1, E2, NS3, NS4, and NS5 regions.

More particularly, a polynucleic acid contained in the composition according to the present invention contains at least 5, preferably 8, or more contiguous nucleotides corresponding to a sequence of contiguous nucleotides selected from at least one of HCV sequences encoding the following new HCV amino acid sequences:

- new sequences spanning amino acid positions 1 to 319 of the Core/E1 region of HCV subtype 2d, type 3 (more particularly new sequences for subtypes 3a and 3c), new type 4

- subtypes (more particularly new sequences for subtypes 4a, 4e, 4f, 4g, 4h, 4i and 4j) and type 5a, as shown in Figure 5;
- new sequences spanning amino acid positions 328 to 546 of the E1/E2 region of HCV subtype 5a as shown in Figure 12;
 - new sequences spanning amino acid positions 1556 to 1764 of the NS3/NS4 region of HCV type 3 (more particularly for new subtypes 3a sequences), and subtype 5a, as shown in Figure 7 or 11;
 - new sequences spanning amino acid positions 2645 to 2757 of the NS5B region of HCV subtype 2d, type 3 (more particularly for new subtypes 3a and 3c), new type 4 subtypes (more particularly subtypes 4a, 4e, 4f, 4g, 4h, 4i and 4j) and subtype 5a, as shown in Figure 2,

Using the LiPA system mentioned above, Brazilian blood donors with high titer type 3 hepatitis C virus, Gabonese patients with high-titer type 4 hepatitis C virus, and a Belgian patient with high-titer HCV type 5 infection were selected. Nucleotide sequences in the core, E1, NS5 and NS4 regions which have not yet been reported before, were analyzed in the frame of the invention. Coding sequences (with the exception of the core region) of any type 4 isolate are reported for the first time in the present invention. The NS5b region was also analyzed for the new type 3 isolates. After having determined the NS5b sequences, comparison with the Ta and Tb subtypes described by Mori et al. (1992) was possible, and the type 3 sequences could be identified as type 3a genotypes. The new type 4 isolates segregated into 10 subtypes, based on homologies obtained in the NS5 and E1 regions. New type 2 and 3 sequences could also be distinguished from previously described type 2 or 3 subtypes from sera collected in Belgium and the Netherlands.

The term "polynucleic acid" refers to a single stranded or double stranded nucleic acid sequence which may contain at least 5 contiguous nucleotides to the complete nucleotide sequence (f.i. at least 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or more contiguous nucleotides). A polynucleic acid which is up till about 100 nucleotides in length is often also referred to as an oligonucleotide. A polynucleic acid may consist of deoxyribonucleotides or ribonucleotides, nucleotide analogues or modified nucleotides, or may have been adapted for therapeutic purposes. A polynucleic acid may also comprise a double stranded cDNA clone which can be used for cloning purposes, or for *in vivo* therapy, or prophylaxis.

The term "polynucleic acid composition" refers to any kind of composition comprising essentially said polynucleic acids. Said composition may be of a diagnostic or a therapeutic

nature.

The expression "nucleotides corresponding to" refers to nucleotides which are homologous or complementary to an indicated nucleotide sequence or region within a specific HCV sequence.

The term "coding region" corresponds to the region of the HCV genome that encodes the HCV polyprotein. In fact, it comprises the complete genome with the exception of the 5' untranslated region and 3' untranslated region.

The term "HCV polyprotein" refers to the HCV polyprotein of the HCV-J isolate (Kato et al., 1990). The adenine residue at position 330 (Kato et al., 1990) is the first residue of the ATG codon that initiates the long HCV polyprotein of 3010 amino acids in HCV-J and other type 1b isolates, and of 3011 amino acids in HCV-1 and other type 1a isolates, and of 3033 amino acids in type 2 isolates HC-J6 and HC-J8 (Okamoto et al., 1992).

This adenine is designated as position 1 at the nucleic acid level, and this methionine is designated as position 1 at the amino acid level, in the present invention. As type 1a isolates contain 1 extra amino acid in the NS5a region, coding sequences of type 1a and 1b have identical numbering in the Core, E1, NS3, and NS4 region, but will differ in the NS5b region as indicated in Table 1. Type 2 isolates have 4 extra amino acids in the E2 region, and 17 or 18 extra amino acids in the NS5 region compared to type 1 isolates, and will differ in numbering from type 1 isolates in the NS3/4 region and NS5b regions as indicated in Table 1.

TABLE 1

	Region	Positions described in the present invention*	Positions described for HCV-J (Kato et al., 1990)	Positions described for HCV-1 (Choo et al., 1991)	Positions described for HC-J6, HC-J8 (Okamoto et al., 1992)
Nucleotides	NS5b	8023/8235 7932/8271	8352/8564 8261/8600	8026/8238 7935/8274	8433/8645 8342/8681
	NS3/4	4664/5292 4664/4730 4892/5292 3856/4209 4936/5292	4993/5621 4993/5059 5221/5621 4185/4528 5265/5621	4664/5292 4664/4730 4892/5292 3856/4209 4936/5292	5017/5645 5017/5083 5245/5645 4209/4762 5289/5645
		coding region of present invention	330/9359	1/9033	342/9439
Amino Acids	NS5b	2675/2745 2645/2757	2675/2745 2645/2757	2676/2746 2646/2758	2698/2768 2668/2780
	NS3/4	1556/1764 1286/1403 1646/1764	1556/1764 1286/1403 1646/1764	1556/1764 1286/1403 1646/1764	1560/1768 1290/1407 1650/1768

Table 1: Comparison of the HCV nucleotide and amino acid numbering system used in the present invention (*) with the numbering used for other prototype isolates. For example, 8352/8564 indicates the region designated by the numbering from nucleotide 8352 to nucleotide 8564 as described by Kato et al. (1990). Since the numbering system of the present invention starts at the polyprotein initiation site, the 329 nucleotides of the 5' untranslated region described by Kato et al. (1990) have to be subtracted, and the corresponding region is numbered from nucleotide 8023 ("8352-329") to 8235 ("8564-329").

The term "HCV type" corresponds to a group of HCV isolates of which the complete genome shows more than 74% homology at the nucleic acid level, or of which the NS5 region between nucleotide positions 7932 and 8271 shows more than 74% homology at the nucleic acid level, or of which the complete HCV polyprotein shows more than 78% homology at the amino acid level, or of which the NS5 region between amino acids at positions 2645 and 2757 shows more than 80% homology at the amino acid level, to polyproteins of the other isolates of the group, with said numbering beginning at the first ATG codon or first methionine of the long HCV polyprotein of the HCV-J isolate (Kato et al., 1990). Isolates belonging to different types of HCV exhibit homologies, over the complete genome, of less than 74% at the nucleic acid level and less than 78% at the amino acid level. Isolates belonging to the same type usually show homologies of about 92 to 95% at the nucleic acid level and 95 to 96% at the amino acid level when belonging to the same subtype, and those belonging to the same type but different subtypes preferably show homologies of about 79% at the nucleic acid level and 85-86% at the amino acid level.

More preferably the definition of HCV types is concluded from the classification of HCV isolates according to their nucleotide distances calculated as detailed below:

(1) based on phylogenetic analysis of nucleic acid sequences in the NS5b region between nucleotides 7935 and 8274 (Choo et al., 1991) or 8261 and 8600 (Kato et al., 1990) or 8342 and 8681 (Okamoto et al., 1991), isolates belonging to the same HCV type show nucleotide distances of less than 0.34, usually less than 0.33, and more usually of less than 0.32, and isolates belonging to the same subtype show nucleotide distances of less than 0.135, usually of less than 0.13, and more usually of less than 0.125, and consequently isolates belonging to the same type but different subtypes show nucleotide distances ranging from 0.135 to 0.34, usually ranging from 0.1384 to 0.2477, and more usually ranging from 0.15 to 0.32, and isolates belonging to different HCV types show nucleotide distances greater than 0.34, usually greater than 0.35, and more usually of greater than 0.358, more usually ranging from 0.1384 to 0.2977.

(2) based on phylogenetic analysis of nucleic acid sequences in the core/E1 region between nucleotides 378 and 957, isolates belonging to the same HCV type show nucleotide distances of less than 0.38, usually of less than 0.37, and more usually of less than 0.364, and isolates belonging to the same subtype show nucleotide distances of less than 0.17, usually of less than 0.16, and more usually of less than 0.15, more usually less than 0.135, more usually less than 0.134, and consequently isolates belonging to the same type but different subtypes show

nucleotide distances ranging from 0.15 to 0.38, usually ranging from 0.16 to 0.37, and more usually ranging from 0.17 to 0.36, more usually ranging from 0.133 to 0.379, and isolates belonging to different HCV types show nucleotide distances greater than 0.34, 0.35, 0.36, usually more than 0.365, and more usually of greater than 0.37,

(3) based on phylogenetic analysis of nucleic acid sequences in the NS3/NS4 region between nucleotides 4664 and 5292 (Choo et al., 1991) or between nucleotides 4993 and 5621 (Kato et al., 1990) or between nucleotides 5017 and 5645 (Okamoto et al., 1991), isolates belonging to the same HCV type show nucleotide distances of less than 0.35, usually of less than 0.34, and more usually of less than 0.33, and isolates belonging to the same subtype show nucleotide distances of less than 0.19, usually of less than 0.18, and more usually of less than 0.17, and consequently isolates belonging to the same type but different subtypes show nucleotide distances ranging from 0.17 to 0.35, usually ranging from 0.18 to 0.34, and more usually ranging from 0.19 to 0.33, and isolates belonging to different HCV types show nucleotide distances greater than 0.33, usually greater than 0.34, and more usually of greater than 0.35.

Table 2 : Molecular evolutionary distances

Region	Core/E1 579 bp	E1 384 bp	NS5B 340 bp	NS5B 222 bp
Isolates*	0.0017 - 0.1347 (0.0750 \pm 0.0245)	0.0026 - 0.2031 (0.0969 \pm 0.0289)	0.0003 - 0.1151 (0.0637 \pm 0.0229)	0.000 - 0.1323 (0.0607 \pm 0.0205)
Subtypes*	0.1330 - 0.3794 (0.2786 \pm 0.0363)	0.1645 - 0.4869 (0.3761 \pm 0.0433)	0.1384 - 0.2977 (0.2219 \pm 0.0341)	0.117 - 0.3538 (0.2391 \pm 0.0399)
Types*	0.3479 - 0.6306 (0.4703 \pm 0.0525)	0.4309 - 0.9561 (0.6308 \pm 0.0928)	0.3581 - 0.6670 (0.4994 \pm 0.0495)	0.3457 - 0.7471 (0.5295 \pm 0.0627)

* Figures created by the PHYLIP program DNADIST are expressed as minimum to maximum (average \pm standard deviation). Phylogenetic distances for isolates belonging to the same subtype ('isolates'), to different subtypes of the same type ('subtypes'), and to different types ('types') are given.

In a comparative phylogenetic analysis of available sequences, ranges of molecular evolutionary distances for different regions of the genome were calculated, based on 19,781

pairwise comparisons by means of the DNA DIST program of the phylogeny inference package PHYLIP version 3.5C (Felsenstein, 1993). The results are shown in Table 2 and indicate that although the majority of distances obtained in each region fit with classification of a certain isolate, only the ranges obtained in the 340bp NS5B-region are non-overlapping and therefor conclusive. However, as was performed in the present invention, it is preferable to obtain sequence information from at least 2 regions before final classification of a given isolate.

Designation of a number to the different types of HCV and HCV types nomenclature is based on chronological discovery of the different types. The numbering system used in the present invention might still fluctuate according to international conventions or guidelines. For example, "type 4" might be changed into "type 5" or "type 6".

The term "subtype" corresponds to a group of HCV isolates of which the complete polyprotein shows a homology of more than 90% both at the nucleic acid and amino acid levels, or of which the NS5 region between nucleotide positions 7932 and 8271 shows a homology of more than 90% at the nucleic acid level to the corresponding parts of the genomes of the other isolates of the same group, with said numbering beginning with the adenine residue of the initiation codon of the HCV polyprotein. Isolates belonging to the same type but different subtypes of HCV show homologies of more than 74% at the nucleic acid level and of more than 78% at the amino acid level.

The term "BR36 subgroup" refers to a group of type 3a HCV isolates (BR36, BR33, BR34) that are 95 %, preferably 95.5 %, most preferably 96 % homologous to the sequences as represented in SEQ ID NO 1, 3, 5, 7, 9, 11 in the NS5b region from position 8023 to 8235.

It is to be understood that extremely variable regions like the E1, E2 and NS4 regions will exhibit lower homologies than the average homology of the complete genome of the polyprotein.

Using these criteria, HCV isolates can be classified into at least 6 types. Several subtypes can clearly be distinguished in types 1, 2, 3 and 4 : 1a, 1b, 2a, 2b, 2c, 2d, 3a, 3b, 4a, 4b, 4c, 4d, 4e, 4f, 4g, 4h, 4i and 4j based on homologies of the 5' UR and coding regions including the part of NS5 between positions 7932 and 8271. An overview of most of the reported isolates and their proposed classification according to the typing system of the present invention as well as other proposed classifications is presented in Table 3.

Table 3**HCV CLASSIFICATION**

	OKA- MOTO	MORI	NAKA O	CHA	PROTOTYPE
1a	I	I	Pt	GI	HCV-1, HCV-H, HC-J1
1b	II	II	KI	GII	HCV-J, HCV-BK, HCV-T, HC-JK1, HC-J4, HCV-CHINA
1c					HC-G9
2a	III	III	K2a	GIII	HC-J6
2b	IV	IV	K2b	GIII	HC-J8
2c					S83, ARG6, ARG8, I10, T983
2d					NE92
3a	V	V	K3	GIV	E-b1, Ta, BR36, BR33, HD10, NZL1
3b		VI	K3	GIV	HCV-TR, Tb
3c					BE98
4a					Z4, GB809-4
4b					Z1
4c					GB116, GB358, GB215, Z6, Z7
4d					DK13
4e					GB809-2, CAM600, CAM736
4f					CAM622, CAM627
4g					GB549
4h					GB438
4i					CAR4/1205
4j					CAR1/501
4k					EG29
5a				GV	SA3, SA4, SA1, SA7, SA11, BE95
6a					HK1, HK2, HK3, HK4

The term "complement" refers to a nucleotide sequence which is complementary to an indicated sequence and which is able to hybridize to the indicated sequences.

The composition of the invention can comprise many combinations. By way of example, the composition of the invention can comprise:

- two (or more) nucleic acids from the same region or,
- two nucleic acids (or more), respectively from different regions, for the same isolate or for different isolates,
- or nucleic acids from the same regions and from at least two different regions (for the same isolate or for different isolates).

The present invention relates more particularly to a polynucleic acid composition as defined above, wherein said polynucleic acid corresponds to a nucleotide sequence selected from any of the following HCV type 3 genomic sequences:

- an HCV genomic sequence having a homology of at least 67%, preferably more than 69%, more preferably 71%, even more preferably more than 73%, or most preferably more than 76% to any of the sequences as represented in SEQ ID NO 13, 15, 17, 19, 21, 23, 25 or 27 (HD10, BR36 or BR33 sequences) in the region spanning positions 417 to 957 of the Core/E1 region as shown in Figure 4;
- an HCV genomic sequence having a homology of at least 65%, preferably more than 67%, preferably more than 69%, even preferably more than 70%, most preferably more than 74% to any of the sequences as represented in SEQ ID NO 13, 15, 17, 19, 21, 23, 25 or 27 (HD10, BR36 or BR33 sequences) in the region spanning positions 574 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence as having a homology of at least 79%, more preferably at least 81%, most preferably more than 83% or more to any of the sequences as represented in SEQ ID NO 147 (representing positions 1 to 346 of the Core region of HVC type 3c, sequence BE98) in the region spanning positions 1 to 378 of the Core region as shown in Figure 3;
- an HCV genomic sequence of HVC type 3a having a homology of at least 74%, more preferably at least 76%, most preferably more than 78% or more to any of the sequences as represented in SEQ ID NO 13, 15, 17, 19, 21, 23, 25 or 27 (HD10, BR36 or BR33 sequences) in the region spanning positions 417 to 957 in the Core/E1 region as shown in Figure 4;
- an HCV genomic sequence of HVC type 3a as having a homology of at least 74%,

preferably more than 76%, most preferably 78% or more to any of the sequences as represented in SEQ ID NO 13, 15, 17, 19, 21, 23, 25 or 27 (HD10, BR36 or BR33 sequences) in the region spanning positions 574 to 957 in the E1 region as shown in Figure 4;

- an HCV genomic sequence as having a homology of more than 73.5%, preferably more than 74%, most preferably 75% homology to the sequence as represented in SEQ ID NO 29 (HCC153 sequence) in the region spanning positions 4664 to 4730 of the NS3 region as shown in figure 6;
- an HCV genomic sequence having a homology of more than 70%, preferably more than 72%, most preferably more than 74% homology to any of the sequences as represented in SEQ ID NO 29, 31, 33, 35, 37 or 39 (HCC153, HD10, BR36 sequences) in the region spanning positions 4892 to 5292 in the NS3/NS4 region as shown in Figure 6 or 10;
- an HCV genomic sequence of the BR36 subgroup of HCV type 3a as having a homology of more than 95%, preferably 95.5%, most preferably 96% homology to any of the sequences as represented in SEQ ID NO 5, 7, 1, 3, 9 or 11 (BR34, BR33, BR36 sequences) in the region spanning positions 8023 to 8235 of the NS5 region as shown in Figure 1;
- an HCV genomic sequence of the BR36 subgroup of HCV type 3a as having a homology of more than 96%, preferably 96.5%, most preferably 97% homology to any of the sequences as represented in SEQ ID NO 5, 7, 1, 3, 9 or 11 (BR34, BR33, BR36 sequences) in the region spanning positions 8023 to 8192 of the NS5B region as shown in Figure 1;
- an HCV genomic sequence of HCV type 3c being characterized as having a homology of more than 79%, more preferably more than 81%, and most preferably more than 83% to the sequence as represented in SEQ ID NO 149 (BE98 sequence) in the region spanning positions 7932 to 8271 in the NS5B region as shown in Figure 1.

Preferentially the above-mentioned genomic HCV sequences depict sequences from the coding regions of all the above-mentioned sequences.

According to the nucleotide distance classification system (with said nucleotide distances being calculated as explained above), said sequences of said composition are selected from:

- an HCV genomic sequence being characterized as having a nucleotide distance of less than 0.44, preferably of less than 0.40, most preferably of less than 0.36 to any of the sequences as represented in SEQ ID NO 13, 15, 17, 19, 21, 23, 25 or 27 in the region

spanning positions 417 to 957 of the Core/E1 region as shown in Figure 4;

- an HCV genomic sequence being characterized having a nucleotide distance of less than 0.53, preferably less than 0.49, most preferably of less than 0.45 to any of the sequences as represented in SEQ ID NO 19, 21, 23, 25 or 27 in the region spanning positions 574 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence characterized having a nucleotide distance of less than 0.15, preferably less than 0.13, and most preferably less than 0.11 to any of the sequences as represented in SEQ ID NO 147 in the region spanning positions 1 to 378 of the Core region as shown in Figure 3;
- an HCV genomic sequence of HVC type 3a being characterized as having a nucleotide distance of less than 0.3, preferably less than 0.26, most preferably of less than 0.22 to any of the sequences as represented in SEQ ID NO 13, 15, 17, 19, 21, 23, 25 or 27 in the region spanning positions 417 to 957 in the Core/E1 region as shown in Figure 4;
- an HCV genomic sequence of HCV type 3a being characterized as having a nucleotide distance of less than 0.35, preferably less than 0.31, most preferably of less than 0.27 to any of the sequences as represented in SEQ ID NO 13, 15, 17, 19, 21, 23, 25 or 27 in the region spanning positions 574 to 957 in the E1 region as shown in Figure 4;
- an HCV genomic sequence of the BR36 subgroup of HCV type 3a being characterized as having a nucleotide sequence of less than 0.0423, preferably less than 0.042, preferably less than 0.0362 to any of the sequences as represented in SEQ ID NO 5, 7, 1, 3, 9 or 11 in the region spanning positions 8023 to 8235 of the NS5 region as shown in Figure 1;
- an HCV genomic sequence of HCV type 3c being characterized as having a nucleotide distance of less than 0.255, preferably of less than 0.25, more preferably of less than 0.21, most preferably of less than 0.17 to the sequence as represented in SEQ ID NO 149 in the region spanning positions 7932 to 8271 in the NS5B region as shown in Figure 1.

In the present application, the E1 sequences encoding the antigenic ectodomain of the E1 protein, which does not overlap the carboxyterminal signal-anchor sequences of E1 disclosed by Cha et al. (1992; WO 92/19743), in addition to the NS4 epitope region, and a part of the NS5 region are disclosed for 4 different isolates: BR33, BR34, BR36, HCC153 and HD10, all belonging to type 3a (SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 35, 37 or 39).

Also within the present invention are new subtype 3c sequences (SEQ ID NO 147, 149 of the isolate BE98 in the Core and NS5 regions (see Figures 3 and 1).

Finally the present invention also relates to a new subtype 3a sequence as represented in SEQ ID NO 217 (see Figure 1)

Also included within the present invention are sequence variants of the polynucleic acids as selected from any of the nucleotide sequences as given in any of the above mentioned SEQ ID numbers, with said sequence variants containing either deletions and/or insertions of one or more nucleotides, mainly at the extremities of oligonucleotides (either 3' or 5'), or substitutions of some non-essential nucleotides by others (including modified nucleotides an/or inosine), for example, a type 1 or 2 sequence might be modified into a type 3 sequence by replacing some nucleotides of the type 1 or 2 sequence with type-specific nucleotides of type 3 as shown in Figure 1 (NS5 region), Figure 3 (Core region), Figure 4 (Core/E1 region), Figure 6 and 10 (NS3/NS4 region).

According to another embodiment, the present invention relates to a polynucleic acid composition as defined above, wherein said polynucleic acids correspond to a nucleotide sequence selected from any of the following HCV type 5 genomic sequences:

- an HCV genomic sequence as having a homology of more than 85 %, preferably more than 86 %, most preferably more than 87 % homology to any of the sequences as represented in SEQ ID NO 41, 43, 45, 47, 49, 51, 53 (PC sequences) or 151 (BE95 sequence) in the region spanning positions 1 to 573 of the Core region as shown in Figure 9 and 3;
- an HCV genomic sequence as having a homology of more than 61 %, preferably more than 63 %, more preferably more than 65 % homology, even more preferably more than 66 % homology and most preferably more than 67 % homology (f.i. 69 and 71 %) to any of the sequences as represented in SEQ ID NO 41, 43, 45, 47, 49, 51, 53 (PC sequences), 153 or 155 (BE95, BE100 sequences) in the region spanning positions 574 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence having a homology of more than 76.5 %, preferably of more than 77 %, most preferably of more than 78 % homology with any of the sequences as represented in SEQ ID NO 55, 57, 197 or 199 (PC sequences) in the region spanning positions 3856 to 4209 of the NS3 region as shown in Figure 6 or 10;
- an HCV genomic sequence having a homology of more than 68 %, preferably of more than 70 %, most preferably of more than 72 % homology with the sequence as represented in SEQ ID NO 157 (BE95 sequence) in the region spanning positions 980 to 1179 of the E1/E2 region as shown in Figure 13;
- an HCV genomic sequence having a homology of more than 57 %, preferably more than

59%, most preferably more than 61% homology to any of the sequences as represented in SEQ ID NO 59 or 61 (PC sequences) in the region spanning positions 4936 to 5296 of the NS4 region as shown in Figure 6 or 10;

- an HCV genomic sequence as having a homology of more than 93%, preferably more than 93.5%, most preferably more than 94% homology to any of the sequences as represented in SEQ ID NO 159 or 161 (BE95 or BE96 sequences) in the region spanning positions 7932 to 8271 of the NSSB region as shown in Figure 1.

Preferentially the above-mentioned genomic HCV sequences depict sequences from the coding regions of all the above-mentioned sequences.

According to the nucleotide distance classification system (with said nucleotide distances being calculated as explained above), said sequences of said composition are selected from:

- a nucleotide distance of less than 0.53, preferably less than 0.51, more preferably less than 0.49 for the E1 region to the type 5 sequences depicted above;
- a nucleotide distance of less than 0.3, preferably less than 0.28, more preferably of less than 0.26 for the Core region to the type 5 sequences depicted above;
- a nucleotide distance of less than 0.072, preferably less than 0.071, more preferably less than 0.070 for the NSSB region to the type 5 sequences as depicted above.

Isolates with similar sequences in the 5'UR to a group of isolates including SA1, SA3, and SA7 described in the 5'UR by Bukh et al. (1992), have been reported and described in the 5'UR and NS5 region as group V by Cha et al. (1992; WO 92/19743). This group of isolates belongs to type 5a as described in the present invention (SEQ ID NO 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 151, 153, 155, 157, 159, 161, 197 and 199).

Also included within the present invention are sequence variants of the polynucleic acids as selected from any of the nucleotide sequences as given in any of the above given SEQ ID numbers with said sequence variants containing either deletion and/or insertions of one or more nucleotides, mainly at the extremities of oligonucleotides (either 3' or 5'), or substitutions of some non-essential nucleotides (i.e. nucleotides not essential to discriminate between different genotypes of HCV) by others (including modified nucleotides an/or inosine), for example, a type 1 or 2 sequence might be modified into a type 5 sequence by replacing some nucleotides of the type 1 or 2 sequence with type-specific nucleotides of type 5 as shown in Figure 3 (Core region), Figure 4 (Core/E1 region), Figure 10 (NS3 / NS4 region), Figure 14 (E1/E2 region).

Another group of isolates including BU74 and BU79 having similar sequences in the 5'UR to isolates including Z6 and Z7 as described in the 5'UR by Bukh et al. (1992), have been described in the 5'UR and classified as a new type 4 by the inventors of this application (Stuyver et al., 1993). Coding sequences, including core, E1 and NS5 sequences of several new Gabonese isolates belonging to this group, are disclosed in the present invention (SEQ ID NO 106, 108, 110, 112, 114, 116, 118, 120 and 122).

According to yet another embodiment, the present invention relates to a composition as defined above, wherein said polynucleic acids correspond to a nucleotide sequence selected from any of the following HCV type 4 genomic sequences:

- an HCV genomic sequence having a homology of more than 66%, preferably more than 68%, most preferably more than 70% homology in the E1 region spanning positions 574 to 957 to any of the sequences as represented in SEQ ID NO 118, 120 or 122 (GB358, GB549, GB809 sequences) as shown in Figure 4;
- an HCV genomic sequence having a homology of more than 71%, preferably more than 72%, most preferably more than 74% homology to any of the sequences as represented in SEQ ID NO 118, 120 or 122 (GB358, GB549, GB809 sequences) in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence having a homology of more than 92%, preferably more than 93%, most preferably more than 94% homology to any of the sequences as represented in SEQ ID NO 163 or 165 (GB809, CAM600 sequences) in the region spanning positions 1 to 378 of the Core/E1 region as shown in Figure 4;
- an HCV genomic sequence (subtype 4c) having a homology of more than 85%, preferably more than 86%, more preferably more than 86.5% homology, most preferably more than 87, more than 88 or more than 89% homology to any of the sequences as represented in SEQ ID NO 183, 185 or 187 (GB116, GB215, GB809 sequences) in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence (subtype 4a) having a homology of more than 81%, preferably more than 83%, most preferably more than 85% homology to the sequence as represented in SEQ ID NO 189 (GB908 sequence) in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence (subtype 4e) having a homology of more than 85%, preferably more than 87%, most preferably more than 89% homology to any of the sequences as represented in SEQ ID NO 167 or 169 (CAM600, GB908 sequences) in the region

- spanning positions 379 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence (subtype 4f) having a homology of more than 79%, preferably more than 81%, most preferably more than 83% homology to any of the sequences as represented in SEQ ID NO 171 or 173 (CAMG22, CAMG27 sequences) in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
 - an HCV genomic sequence (subtype 4g) having a homology of more than 84%, preferably more than 86%, most preferably more than 88% homology to the sequence as represented in SEQ ID NO 175 (GB549 sequence) in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
 - an HCV genomic sequence (subtype 4h) having a homology of more than 83%, preferably more than 85%, most preferably more than 87% homology to the sequence as represented in SEQ ID NO 177 (GB438 sequence) in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
 - an HCV genomic sequence (subtype 4i) as having a homology of more than 76%, preferably more than 78%, most preferably more than 80% homology to the sequence as represented in SEQ ID NO 179 (CAR4/1205 sequence) in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
 - an HCV genomic sequence (subtype 4j?) having a homology of more than 84%, preferably more than 86%, most preferably more than 88% homology to the sequence as represented in SEQ ID NO 181 (CAR4/901 sequence) in the region spanning positions 379 to 957 of the E1 region as shown in figure 4;
 - an HCV genomic sequence as having a homology of more than 73%, preferably more than 75%, most preferably more than 77% homology to any of the sequences as represented in SEQ ID NO 106, 108, 110, 112, 114, or 116 (GB48, GB116, GB215, GB358, GB549, GB809 sequences) in the region spanning positions 7932 to 8271 of the NS5 region as shown in figure 1;
 - an HCV genomic sequence (subtype 4c) having a homology of more than 88%, preferably more than 89%, most preferably more than 90% homology to any of the sequences as represented in SEQ ID NO 106, 108, 110, or 112 (GB48, GB116, GB215, GB358 sequences) in the region spanning positions 7932 to 8271 of the NS5 region as shown in Figure 1;
 - an HCV genomic sequence (subtype 4e) having a homology of more than 88%, preferably more than 89%, most preferably more than 90% homology to any of the sequences as

represented in SEQ ID NO 116 or 201 (GB809 or CAM 600 sequences) in the region spanning positions 7932 to 8271 of the NS5 region as shown in Figure 1;

- an HCV genomic sequence (subtype 4f) having a homology of more than 87%, preferably more than 89%, most preferably more than 90% homology to the sequence as represented in SEQ ID NO 203 (CAMG22 sequence) in the region spanning positions 7932 to 8271 of the NS5 region as shown in Figure 1;
- an HCV genomic sequence (subtype 4g) as having a homology of more than 85%, preferably more than 87%, most preferably more than 89% homology to the sequence as represented in SEQ ID NO 114 (GB549 sequence) in the region spanning positions 7932 to 8271 of the NS5 region as shown in Figure 1;
- an HCV genomic sequence (subtype 4h) as having a homology of more than 86%, preferably more than 87%, more preferably more than 88% homology, more preferably more than 89% homology to the sequence as represented in SEQ ID NO 207 (GB437 sequence) in the region spanning positions 7932 to 8271 of the NS5 region as shown in Figure 1;
- an HCV genomic sequence (subtype 4i) having a homology of more than 84%, preferably more than 86%, most preferably more than 88% homology to the sequence as represented in SEQ ID NO 209 (CAR4/1205 sequence) in the region spanning positions 7932 to 8271 of the NS5 region as shown in figure 1;
- an HCV genomic sequence (subtype 4j) having a homology of more than 81%, preferably more than 83%, most preferably more than 85% homology to the sequence as represented in SEQ ID NO 211 (CAR1/501 sequence) in the region spanning positions 7932 to 8271 of the NS5 region as shown in figure 1.

Preferentially the above-mentioned genomic HCV sequences depict sequences from the coding regions of all the above-mentioned sequences.

According to the nucleotide distance classification system (with said nucleotide distances being calculated as explained above), said sequences of said composition are selected from:

- an HCV genomic sequence (type 4) being characterized as having a nucleotide distance of less than 0.52, 0.50, 0.4880, 0.46, 0.44, 0.43 or most preferably less than 0.42 in the region spanning positions 574 to 957 to any of the sequences as represented in SEQ ID NO 118, 120 or 122 in the region spanning positions 1 to 957 of the Core/E1 region as shown in Figure 4;
- an HCV genomic sequence (type 4) being characterized as having a nucleotide distance of

- less than 0.39, 0.36 0.34 0.32 or most preferably less than 0.31 to any of the sequences as represented in SEQ ID NO 118, 120 or 122 in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
- an HCV genomic sequence (subtype 4c) being characterized as having a nucleotide distance of less than 0.27, 0.26, 0.24, 0.22, 0.20, 0.18, 0.17, 0.162, 0.16 or most preferably less than 0.15 to any of the sequences as represented in SEQ ID NO 183, 185 or 187 in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
 - an HCV genomic sequence (subtype 4a) being characterized as having a nucleotide distance of less than 0.30, 0.28, 0.26, 0.24, 0.22, 0.21 or most preferably of less than 0.205 to the sequence as represented in SEQ ID NO 189 in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
 - an HCV genomic sequence (subtype 4e) being characterized as having a nucleotide distance of less than 0.26, 0.25, 0.23, 0.21, 0.19, 0.17, 0.165, most preferably less than 0.16 to any of the sequences as represented in SEQ ID NO 167 or 169 in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
 - an HCV genomic sequence (subtype 4f) being characterized as having a nucleotide distance of less than 0.26, 0.24, 0.22, 0.20, 0.18, 0.16, 0.15 or most preferably less than 0.14 to any of the sequences as represented in SEQ ID NO 171 or 173 in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
 - an HCV genomic sequence (subtype 4g) being characterized as having a nucleotide distance of less than 0.20, 0.19, 0.18, 0.17 or most preferably of less than 0.16 to the sequence as represented in SEQ ID NO 175 in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
 - an HCV genomic sequence (subtype 4h) being characterized as having a nucleotide distance of less than 0.20, 0.19, 0.18, 0.17 and most preferably of less than 0.16 to the sequence as represented in SEQ ID NO 177 in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
 - an HCV genomic sequence (subtype 4i) being characterized as having a nucleotide distance of less than 0.27, 0.25, 0.23, 0.21 and preferably less than 0.16 to the sequence as represented in SEQ ID NO 179 in the region spanning positions 379 to 957 of the E1 region as shown in Figure 4;
 - an HCV genomic sequence (subtype 4j?) being characterized as having a nucleotide distance of less than 0.19, 0.18, 0.17, 0.165 and most preferably of less than 0.16 to the

sequence as represented in SEQ ID NO 181 in the region spanning positions 379 to 957 of the E1 region as shown in figure 4;

- an HCV genomic sequence (type 4) being characterized as having a nucleotide distance of less than 0.35, 0.34, 0.32 and most preferably of less than 0.30 to any of the sequences as represented in SEQ ID NO 106, 108, 110, 112, 114, or 116 in the region spanning positions 7932 to 8271 of the NS5 region as shown in figure 1;
- an HCV genomic sequence (subtype 4c) being characterized as having a nucleotide distance of less than 0.18, 0.16, 0.14, 0.135, 0.13, 0.1275 or most preferably less than 0.125 to any of the sequences as represented in SEQ ID NO 106, 108, 110, or 112 in the region spanning positions 7932 to 8271 of the NS5 region as shown in Figure 1;
- an HCV genomic sequence (subtype 4e) being characterized as having a nucleotide distance of less than 0.15, 0.14, 0.135, 0.13 and most preferably of less than 0.125 to any of the sequences as represented in SEQ ID NO 116 or 201 in the region spanning positions 7932 to 8271 of the NS5 region as shown in Figure 1;
- an HCV genomic sequence (subtype 4f) being characterized as having a nucleotide distance of less than 0.15, 0.14, 0.135, 0.13 or most preferably less than 0.125 to the sequence as represented in SEQ ID NO 203 in the region spanning positions 7932 to 8271 of the NS5 region as shown in Figure 1;
- an HCV genomic sequence (subtype 4g) being characterized as having a nucleotide distance of less than 0.17, 0.16, 0.15, 0.14, 0.13 or most preferably less than 0.125 to the sequence as represented in SEQ ID NO 114 in the region spanning positions 7932 to 8271 of the NS5 region as shown in Figure 1;
- an HCV genomic sequence (subtype 4h) being characterized as having a nucleotide distance of less than 0.155, 0.15, 0.145, 0.14, 0.135, 0.13 or most preferably less than 0.125 to the sequence as represented in SEQ ID NO 207 in the region spanning positions 7932 to 8271 of the NS5 region as shown in Figure 1;
- an HCV genomic sequence (subtype 4i) being characterized as having a nucleotide distance of less than 0.17, 0.16, 0.15, 0.14, 0.13 or most preferably of less than 0.125 to the sequence as represented in SEQ ID NO 209 in the region spanning positions 7932 to 8271 of the NS5 region as shown in figure 1;
- an HCV genomic sequence (subtype 4j) being characterized as having a nucleotide distance of less than 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13 and most preferably of less than 0.125 to the sequence as represented in SEQ ID NO 211 in the region spanning

positions 7932 to 8271 of the NSS region as shown in figure 1.

Also included within the present invention are sequence variants of the polynucleic acids as selected from any of the nucleotide sequences as given in any of the above given SEQ ID numbers with said sequence variants containing either deletion and/or insertions of one or more nucleotides, mainly at the extremities of oligonucleotides (either 3' or 5'), or substitutions of some non-essential nucleotides (i.e. nucleotides not essential to discriminate between different genotypes of HCV) by others (including modified nucleotides an/or inosine), for example, a type 1 or 2 sequence might be modified into a type 4 sequence by replacing some nucleotides of the type 1 or 2 sequence with type-specific nucleotides of type 4 as shown in Figure 3 (Core region), Figure 4 (Core/E1 region), Figure 10 (NS3 / NS4 region), Figure 14 (E1/E2 region).

The present invention also relates to a sequence as represented in SEQ ID NO 193 (GB724 sequence).

After aligning NS5 or E1 sequences of GB48, GB, 116, GB215, GB358, GB549 and GB809, these isolates clearly segregated into 3 subtypes within type 4 : GB48, GB116, GB215 and GB358 belong to the sybtype designated 4c, GB549 to subtype 4g and GB809 to subtype 4e. In NS5, GB809 (subtype 4e) showed a higher nucleic acids homology to subtype 4c isolates (85.6 - 86.8%) than to GB549 (subtype 4g, 79.7%), while GB549 showed similar homologies to both other subtypes (78.8 to 80% to subtype 4c and 79.7% to subtype 4e). In E1, subtype 4c showed equal nucleic acid homologies of 75.2% to subtypes 4g and 4e while 4g and 4e were 78.4% homologous. At the amino acid level however, subtype 4e showed a normal homology to subtype 4c (80.2%), while subtype 4g was more homologous to 4c (83.3%) and 4e (84.1%).

According to yet another embodiment, the present invention relates to a composition as defined above, wherein said polynucleic acids correspond to a nucleotide sequence selected from any of the following HCV type 2d genomic sequences:

- an HCV genomic sequence as having a homology of more than 78%, preferably more than 80%, most preferably more than 82% homology to the sequence as represented in SEQ ID NO (NE92) 143 in the region spanning positions 379 to 957 of the Core/E1 region as shown in Figure 4;
- an HCV genomic sequence as having a homology of more than 74%, preferably more than 76%, most preferably more than 78% homology to the sequence as represented in SEQ ID NO 143 (NE92) in the region spanning positions 574 to 957 as shown in Figure 4;

- an HCV genomic sequence as having a homology of more than 87%, preferably more than 89%, most preferably more than 91% homology to the sequence as represented in SEQ ID NO 145 (NE92) in the region spanning positions 7932 to 8271 of the NS5B region as shown in Figure 1.

Preferentially the above-mentioned genomic HCV sequences depict sequences from the coding regions of all the above-mentioned sequences.

According to the nucleotide distance classification system (with said nucleotide distances being calculated as explained above), said sequences of said composition are selected from:

- a nucleotide distance of less than 0.32, preferably less than 0.31, more preferably less than 0.30 for the E1 region (574 to 957) to any of the above specified sequences;
- a nucleotide distance of less than 0.08, preferably less than 0.07, more preferably less than 0.06 for the Core region (1 to 378) to any of the above given sequences
- a nucleotide distance of less than 0.15, preferentially less than 0.13, more preferentially less than 0.12 for the NS5B region to any of the above-specified sequences.

Polynucleic acid sequences according to the present invention which are homologous to the sequences as represented by a SEQ ID NO can be characterized and isolated according to any of the techniques known in the art, such as amplification by means of type or subtype specific primers, hybridization with type or subtype specific probes under more or less stringent conditions, serological screening methods (see examples 4 and 11) or via the LiPA typing system.

Polynucleic acid sequences of the genomes indicated above from regions not yet depicted in the present examples, figures and sequence listing can be obtained by any of the techniques known in the art, such as amplification techniques using suitable primers from the type or subtype specific sequences of the present invention.

The present invention relates also to a composition as defined above, wherein said polynucleic acid is liable to act as a primer for amplifying the nucleic acid of a certain isolate belonging to the genotype from which the primer is derived.

An example of a primer according to this embodiment of the invention is HCP_r 152 as shown in table 7 (SEQ ID NO 79).

The term "primer" refers to a single stranded DNA oligonucleotide sequence capable of acting as a point of initiation for synthesis of a primer extension product which is complementary to the nucleic acid strand to be copied. The length and the sequence of the primer must be such that they allow to prime the synthesis of the extension products.

Preferably the primer is about 5-50 nucleotides. Specific length and sequence will depend on the complexity of the required DNA or RNA targets, as well as on the conditions of primer use such as temperature and ionic strength.

The fact that amplification primers do not have to match exactly with corresponding template sequence to warrant proper amplification is amply documented in the literature (Kwok et al., 1990).

The amplification method used can be either polymerase chain reaction (PCR; Saiki et al., 1988), ligase chain reaction (LCR; Landgren et al., 1988; Wu & Wallace, 1989; Barany, 1991), nucleic acid sequence-based amplification (NASBA; Guatelli et al., 1990; Compton, 1991), transcription-based amplification system (TAS; Kwok et al., 1989), strand displacement amplification (SDA; Duck, 1990; Walker et al., 1992) or amplification by means of Q β replicase (Lizardi et al., 1988; Lomeli et al., 1989) or any other suitable method to amplify nucleic acid molecules using primer extension. During amplification, the amplified products can be conveniently labelled either using labelled primers or by incorporating labelled nucleotides. Labels may be isotopic (^{32}P , ^{35}S , etc.) or non-isotopic (biotin, digoxigenin, etc.). The amplification reaction is repeated between 20 and 80 times, advantageously between 30 and 50 times.

The present invention also relates to a composition as defined above, wherein said polynucleic acid is able to act as a hybridization probe for specific detection and/or classification into types of a nucleic acid containing said nucleotide sequence, with said oligonucleotide being possibly labelled or attached to a solid substrate.

The term "probe" refers to single stranded sequence-specific oligonucleotides which have a sequence which is complementary to the target sequence of the HCV genotype(s) to be detected.

Preferably, these probes are about 5 to 50 nucleotides long, more preferably from about 10 to 25 nucleotides.

The term "solid support" can refer to any substrate to which an oligonucleotide probe can be coupled, provided that it retains its hybridization characteristics and provided that the background level of hybridization remains low. Usually the solid substrate will be a microtiter plate, a membrane (e.g. nylon or nitrocellulose) or a microsphere (bead). Prior to application to the membrane or fixation it may be convenient to modify the nucleic acid probe in order to facilitate fixation or improve the hybridization efficiency. Such modifications may encompass homopolymer tailing, coupling with different reactive groups such as aliphatic

groups, NH₂ groups, SH groups, carboxylic groups, or coupling with biotin or haptens.

The present invention also relates to the use of a composition as defined above for detecting the presence of one or more HCV genotypes, more particularly for detecting the presence of a nucleic acid of any of the HCV genotypes having a nucleotide sequence as defined above, present in a biological sample liable to contain them, comprising at least the following steps:

- (i) possibly extracting sample nucleic acid,
- (ii) possibly amplifying the nucleic acid with at least one of the primers as defined above or any other HCV subtype 2d, HCV type 3, HCV type 4, HCV type 5 or universal HCV primer,
- (iii) hybridizing the nucleic acids of the biological sample, possibly under denatured conditions, and with said nucleic acids being possibly labelled during or after amplification, at appropriate conditions with one or more probes as defined above, with said probes being preferably attached to a solid substrate,
- (iv) washing at appropriate conditions,
- (v) detecting the hybrids formed,
- (vi) inferring the presence of one or more HCV genotypes present from the observed hybridization pattern.

Preferably, this technique could be performed in the Core or NS5B region.

The term "nucleic acid" can also be referred to as analyte strand and corresponds to a single- or double-stranded nucleic acid molecule. This analyte strand is preferentially positive- or negative stranded RNA, cDNA or amplified cDNA.

The term "biological sample" refers to any biological sample (tissue or fluid) containing HCV nucleic acid sequences and refers more particularly to blood serum or plasma samples.

The term "HCV subtype 2d primer" refers to a primer which specifically amplifies HCV subtype 2d sequences present in a sample (see Examples section and figures).

The term "HCV type 3 primer" refers to a primer which specifically amplifies HCV type 3 sequences present in a sample (see Examples section and figures).

The term "HCV type 4 primer" refers to a primer which specifically amplifies HCV type 4 genomes present in a sample.

The term "universal HCV primer" refers to oligonucleotide sequences complementary to any of the conserved regions of the HCV genome.

The term "HCV type 5 primer" refers to a primer which specifically amplifies HCV type

5 genomes present in a sample. The term "universal HCV primer" refers to oligonucleotide sequences complementary to any of the conserved regions of the HCV genome.

The expression "appropriate" hybridization and washing conditions are to be understood as stringent and are generally known in the art (e.g. Maniatis et al., Molecular Cloning: A Laboratory Manual, New York, Cold Spring Harbor Laboratory, 1982).

However, according to the hybridization solution (SSC, SSPE, etc.), these probes should be hybridized at their appropriate temperature in order to attain sufficient specificity.

The term "labelled" refers to the use of labelled nucleic acids. This may include the use of labelled nucleotides incorporated during the polymerase step of the amplification such as illustrated by Saiki et al. (1988) or Bej et al. (1990) or labelled primers, or by any other method known to the person skilled in the art.

The process of the invention comprises the steps of contacting any of the probes as defined above, with one of the following elements:

- either a biological sample in which the nucleic acids are made available for hybridization,
- or the purified nucleic acids contained in the biological sample
- or a single copy derived from the purified nucleic acids,
- or an amplified copy derived from the purified nucleic acids, with said elements or with said probes being attached to a solid substrate.

The expression "inferring the presence of one or more HCV genotypes present from the observed hybridization pattern" refers to the identification of the presence of HCV genomes in the sample by analyzing the pattern of binding of a panel of oligonucleotide probes. Single probes may provide useful information concerning the presence or absence of HCV genomes in a sample. On the other hand, the variation of the HCV genomes is dispersed in nature, so rarely is any one probe able to identify uniquely a specific HCV genome. Rather, the identity of an HCV genotype may be inferred from the pattern of binding of a panel of oligonucleotide probes, which are specific for (different) segments of the different HCV genomes. Depending on the choice of these oligonucleotide probes, each known HCV genotype will correspond to a specific hybridization pattern upon use of a specific combination of probes. Each HCV genotype will also be able to be discriminated from any other HCV genotype amplified with the same primers depending on the choice of the oligonucleotide probes. Comparison of the generated pattern of positively hybridizing probes for a sample containing one or more unknown HCV sequences to a scheme of expected

hybridization patterns, allows one to clearly infer the HCV genotypes present in said sample.

The present invention thus relates to a method as defined above, wherein one or more hybridization probes are selected from any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59 or 61, 106, 108, 110, 112, 114, 116, 118, 120, 122, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 198, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 222, 269 or sequence variants thereof, with said sequence variants containing deletions and/or insertions of one or more nucleotides, mainly at their extremities (either 3' or 5'), or substitutions of some non-essential nucleotides (i.e. nucleotides not essential to discriminate between genotypes) by others (including modified nucleotides or inosine), or with said variants consisting of the complement of any of the above-mentioned oligonucleotide probes, or with said variants consisting of ribonucleotides instead of deoxyribonucleotides, all provided that said variant probes can be caused to hybridize with the same specificity as the oligonucleotide probes from which they are derived.

In order to distinguish the amplified HCV genomes from each other, the target polynucleic acids are hybridized to a set of sequence-specific DNA probes targetting HCV genotypic regions located in the HCV polynucleic acids.

Most of these probes target the most type-specific regions of HCV genotypes, but some can be caused to hybridize to more than one HCV genotype.

According to the hybridization solution (SSC, SSPE, etc.), these probes should be stringently hybridized at their appropriate temperature in order to attain sufficient specificity. However, by slightly modifying the DNA probes, either by adding or deleting one or a few nucleotides at their extremities (either 3' or 5'), or substituting some non-essential nucleotides (i.e. nucleotides not essential to discriminate between types) by others (including modified nucleotides or inosine) these probes or variants thereof can be caused to hybridize specifically at the same hybridization conditions (i.e. the same temperature and the same hybridization solution). Also changing the amount (concentration) of probe used may be beneficial to obtain more specific hybridization results. It should be noted in this context, that probes of the same length, regardless of their GC content, will hybridize specifically at approximately the same temperature in TMAcI solutions (Jacobs et al., 1988).

Suitable assay methods for purposes of the present invention to detect hybrids formed between the oligonucleotide probes and the nucleic acid sequences in a sample may comprise

any of the assay formats known in the art, such as the conventional dot-blot format, sandwich hybridization or reverse hybridization. For example, the detection can be accomplished using a dot blot format, the unlabelled amplified sample being bound to a membrane, the membrane being incorporated with at least one labelled probe under suitable hybridization and wash conditions, and the presence of bound probe being monitored.

An alternative and preferred method is a "reverse" dot-blot format, in which the amplified sequence contains a label. In this format, the unlabelled oligonucleotide probes are bound to a solid support and exposed to the labelled sample under appropriate stringent hybridization and subsequent washing conditions. It is to be understood that also any other assay method which relies on the formation of a hybrid between the nucleic acids of the sample and the oligonucleotide probes according to the present invention may be used.

According to an advantageous embodiment, the process of detecting one or more HCV genotypes contained in a biological sample comprises the steps of contacting amplified HCV nucleic acid copies derived from the biological sample, with oligonucleotide probes which have been immobilized as parallel lines on a solid support.

According to this advantageous method, the probes are immobilized in a Line Probe Assay (LiPA) format. This is a reverse hybridization format (Saiki et al., 1989) using membrane strips onto which several oligonucleotide probes (including negative or positive control oligonucleotides) can be conveniently applied as parallel lines.

The invention thus also relates to a solid support, preferably a membrane strip, carrying on its surface, one or more probes as defined above, coupled to the support in the form of parallel lines.

The LiPA is a very rapid and user-friendly hybridization test. Results can be read 4 h. after the start of the amplification. After amplification during which usually a non-isotopic label is incorporated in the amplified product, and alkaline denaturation, the amplified product is contacted with the probes on the membrane and the hybridization is carried out for about 1 to 1.5 h hybridized polynucleic acid is detected. From the hybridization pattern generated, the HCV type can be deduced either visually, but preferably using dedicated software. The LiPA format is completely compatible with commercially available scanning devices, thus rendering automatic interpretation of the results very reliable. All those advantages make the LiPA format liable for the use of HCV detection in a routine setting. The LiPA format should be particularly advantageous for detecting the presence of different HCV genotypes.

The present invention also relates to a method for detecting and identifying novel HCV

genotypes, different from the known HCV genomes, comprising the steps of:

- determining to which HCV genotype the nucleotides present in a biological sample belong, according to the process as defined above,
- in the case of observing a sample which does not generate a hybridization pattern compatible with those defined in Table 3, sequencing the portion of the HCV genome sequence corresponding to the aberrantly hybridizing probe of the new HCV genotype to be determined.

The present invention also relates to the use of a composition as defined above, for detecting one or more genotypes of HCV present in a biological sample liable to contain them, comprising the steps of:

- (i) possibly extracting sample nucleic acid,
- (ii) amplifying the nucleic acid with at least one of the primers as defined above,
- (iii) sequencing the amplified products
- (iv) inferring the HCV genotypes present from the determined sequences by comparison to all known HCV sequences.

The present invention also relates to a composition consisting of or comprising at least one peptide or polypeptide comprising a contiguous sequence of at least 5 amino acids corresponding to a contiguous amino acid sequence encoded by at least one of the HCV genomic sequences as defined above, having at least one amino acid differing from the corresponding region of known HCV (type 1 and/or type 2 and/or type 3) polypeptide sequences as shown in Table 3, or muteins thereof.

It is to be noted that, at the level of the amino acid sequence, an amino acid difference (with respect to known HCV amino acid sequences) is necessary, which means that the polypeptides of the invention correspond to polynucleic acids having a nucleotide difference (with known HCV polynucleic acid sequences) involving an amino acid difference.

The new amino acid sequences, as deduced from the disclosed nucleotide sequences (see SEQ ID NO 1 to 62 and 106 to 123 and 143 to 218, 223 and 270), show homologies of only 59.9 to 78% with prototype sequences of type 1 and 2 for the NS4 region, and of only 53.9 to 68.8% with prototype sequences of type 1 and 2 for the E1 region. As the NS4 region is known to contain several epitopes, for example characterized in patent application EP-A-0 489 968, and as the E1 protein is expected to be subject to immune attack as part of the viral envelope and expected to contain epitopes, the NS4 and E1 epitopes of the new type 3, 4 and 5 isolates will consistently differ from the epitopes present in type 1 and 2 isolates. This is

exemplified by the type-specificity of NS4 synthetic peptides as presented in example 4, and the type-specificity of recombinant E1 proteins in example 11.

After aligning the new subtype 2d, type 3, 4 and 5 (see SEQ ID NO 1 to 62 and 106 to 123 and 143 to 218, 223 and 270) amino acid sequences with the prototype sequences of type 1a, 1b, 2a, and 2b, type- and subtype-specific variable regions can be delineated as presented in Figure 5 and 7.

As to the muteins derived from the polypeptides of the invention, Table 4 gives an overview of the amino acid substitutions which could be the basis of some of the muteins as defined above.

The peptides according to the present invention contain preferably at least 5 contiguous HCV amino acids, preferably however at least 8 contiguous amino acids, at least 10 or at least 15 (for instance at least 9, 11, 12, 13, 14, 20 or 25 amino acids) of the new HCV sequences of the invention.

TABLE 4

Amino acids	Synonymous groups
Ser (S)	Ser, Thr, Gly, Asn
Arg (R)	Arg, His, Lys, Glu, Gln
Leu (L)	Leu; Ile, Met, Phe, Val, Tyr
Pro (P)	Pro, Ala, Thr, Gly
Thr (T)	Thr, Pro, Ser, Ala, Gly, His, Gln
Ala (A)	Ala, Pro, Gly, Thr
Val (V)	Val, Met, Ile, Tyr, Phe, Leu, Val
Gly (G)	Gly, Ala, Thr, Pro, Ser
Ile (I)	Ile, Met, Leu, Phe, Val, Ile, Tyr
Phe (F)	Phe, Met, Tyr, Ile, Leu, Trp, Val
Tyr (Y)	Tyr, Phe, Trp, Met, Ile, Val, Leu
Cys (C)	Cys, Ser, Thr, Met
His (H)	His, Gln, Arg, Lys, Glu, Thr
Gln (Q)	Gln, Glu, His, Lys, Asn, Thr, Arg
Asn (N)	Asn, Asp, Ser, Gln
Lys (K)	Lys, Arg, Glu, Gln, His
Asp (D)	Asp, Asn, Glu, Gln
Glu (E)	Glu, Gln, Asp, Lys, Asn, His, Arg
Met (M)	Met, Ile, Leu, Phe, Val

The polypeptides of the invention, and particularly the fragments, can be prepared by classical chemical synthesis.

The synthesis can be carried out in homogeneous solution or in solid phase.

For instance, the synthesis technique in homogeneous solution which can be used is the one described by Houbenweyl in the book entitled "Methode der organischen chemie" (Method of organic chemistry) edited by E. Wunsh, vol. 15-I et II. THIEME, Stuttgart 1974.

The polypeptides of the invention can also be prepared in solid phase according to the methods described by Atherton and Shepard in their book entitled "Solid phase peptide synthesis" (IRL Press, Oxford, 1989).

The polypeptides according to this invention can be prepared by means of recombinant DNA techniques as described by Maniatis et al., Molecular Cloning: A Laboratory Manual, New York, Cold Spring Harbor Laboratory, 1982).

The present invention relates particularly to a polypeptide or peptide composition as defined above, wherein said contiguous sequence contains in its sequence at least one of the following amino acid residues:

L7, Q43, M44, S60, R67, Q70, T71, A79, A87, N106, K115, A127, A190, S130, V134, G142, I144, E152, A157, V158, P165, S177 or Y177, I178, V180 or E180 or F182, R184, I186, H187, T189, A190, S191 or G191, Q192 or L192 or I192 or V192 or E192, N193 or H193 or P193, W194 or Y194, H195, A197 or I197 or V197 or T197, V202, I203 or L203, Q208, A210, V212, F214, T216, R217 or D217 or E217 or V217, H218 or N218, H219 or V219 or L219, L227 or I227, M231 or E231 or Q231, T232 or D232 or A232 or K232, Q235 or I235, A237 or T237, I242, I246, S247, S248, V249, S250 or Y250, I251 or V251 or M251 or F251, D252, T254 or V254, L255 or V255, E256 or A256, M258 or F258 or V258, A260 or Q260 or S260, A261, T264 or Y264, M265, I266 or A266, A267, G268 or T268, F271 or M271 or V271, I277, M280 or H280, I284 or A284 or L84, V274, V291, N292 or S292, R293 or I293 or Y293, Q294 or R294, L297 or I297 or Q297, A299 or K299 or Q299, N303 or T303, T308 or L308, T310 or F310 or A310 or D310 or V310, L313, G317 or Q317, L333, S351, A358, A359, A363, S364, A366, T369, L373, F376, Q386, I387, S392, I399, F402, I403, R405, D454, A461, A463, T464, K484, Q500, E501, S521, K522, H524, N528, S531, S532, V534, F536, F537, M539, I546, C1282, A1283, H1310, V1312, Q1321, P1368, V1372, V1373, K1405, Q1406, S1409, A1424, A1429, C1435, S1436, S1456, H1496, A1504, D1510, D1529, I1543, N1567, D1556, N1567, M1572, Q1579, L1581, S1583, F1585, V1595, E1606 or T1606, M1611, V1612 or L1612, P1630, C1636, P1651, T1656 or I1656, L1663, V1667, V1677, A1681, H1685, E1687, G1689, V1695, A1700, Q1704, Y1705, A1713, A1714 or S1714, M1718, D1719, A1721 or T1721, R1722, A1723 or V1723, H1726 or G1726, E1730, V1732, F1735, I1736, S1737, R1738, T1739, G1740, Q1741, K1742, Q1743, A1744, T1745, L1746, E1747 or K1747, I1749, A1750, T1751 or A1751, V1753, N1755, K1756, A1757, P1758, A1759, H1762, T1763, Y1764, P2645, A2647, K2650, K2653 or L2653, S2664, N2673, F2680, K2681, L2686, H2692, Q2695 or L2695 or I2695, V2712, F2715, V2719 or Q2719, T2722, T2724, S2725, R2726, G2729, Y2735, H2739, I2748, G2746 or I2746, I2748, P2752 or K2752, P2754 or T2754, T2757 or P2757,

with said notation being composed of a letter representing the amino acid residue by its one-letter code, and a number representing the amino acid numbering according to Kato et al., 1990 as shown in Table 1 (comparison with other isolates). See also the numbering in Figures 2, 5, 7, and 11 (alignment amino acid sequences).

Within the group of unique and new amino acid residues of the present invention, the following residues were found to be specific for the following types of HCV according to the

HCV classification system used in the present invention:

- Q208, R217, E231, I235, I246, T264, I266, A267, F271, K299, L2686, Q2719 which are specific for the HCV subtype 2d sequences of the present invention as shown in Fig. 5 and 2;
- Q43, S60, R67, F182, I186, H187, A190, S191, L192, W194, V202, L203, V219, Q231, D232, A237, T254, M280, Q299, T303, L308, and/or L313 which are specific for the Core/E1 region of HCV type 3 of the invention as shown in Fig. 5;
- D1556, Q1579, L1581, S1584, F1585, E1606, V1612, P1630, C1636, T1656, L1663, H1685, E1687, G1689, V1695, Y1705, A1713, A1714, A1721, V1723, H1726, R1738, Q1743, A1744, E1747, I1749, A1751, A1759 and/or H1762 which are specific for the NS3/4 region of HCV type 3 sequences of the invention as shown in Fig. 7;
- K2665, D2666, R2670 which are specific for the NS5B region of HCV type 3 of the invention as shown in Fig. 2;
- L7, A79, A127, S130, E152, V158, S177 or Y177, V180 or E180, R184, T189, Q192 or E192 or I192, N193 or H193, I197 or V197, I203, A210, V212, E217, H218, H219, L227, A232, V249, I251 or M251, D252, L255 or V255, E256, M258 or V258 or F258, A260 or Q260, M265, T268, V271, V274, M280, I284, N292 or S292, Q294, L297 or I297, T308, A310 or D310 or V310 or T310, and G317 which are specific for the core/E1 region of HCV type 4 sequences of the present invention as shown in Fig. 5;
- P2645, K2650, K2653, G2656, V2658, T2668, N2673 or N2673, K2681, H2686, D2691, L2692, Q2695 or L2695 or I2695, Y2704, V2712, F2715, V2719, I2722, S2725, G2729, Y2735, G2746 or I2746, P2752 or K2752, Q2753, P2754 or T2754, T2757 or P2757 which are specific for the NS5B region of the HCV type 4 sequences of the present invention as shown in Fig. 2;
- M44, Q70, A87, N106, K115, V137, G142, P165, I178, F251, A299, N303, Q317 which are specific for the Core/E1 region of the HCV type 4 sequences of the present invention as shown in Fig. 5;
- L333, S351, A358, A359, A363, S364, A366, T369, L373, F376, Q386, I387, S392, I399, F102, I403, R405, D454, A461, A463, T464, K484, Q500, E501, S521, K522, H524, N528, S532, V534, F537, M539, I546 which are specific for

the E1/E2 region of the HCV type 5 sequences of the present invention as shown in Fig. 12;

- C1282, A1283, V1312, Q1321, P1368, V1372, K1405, Q1406, S1409, A1424, A1429, C1435, S1436, S1456, H1496, A1504, D1510, D1529, I1543, N1567, M1572, V1595, T1606, M1611, L1612, I1656, V1667, A1681, A1700, A1713, S1714, M1718, D1719, T1721, R1722, A1723, G1726, F1735, I1736, S1737, T1739, G1740, K1742, T1745, L1746, K1747, A1750, V1753, N1755, A1757, D1758, T1763, and Y1764 which are specific for the NS3/NS4 region of HCV type 5 sequences of the invention as shown in Fig. 7;
- A2647, L2653, S2674, F2680, T2724, R2726, Y2730, H2739 which are specific for the NS5B region of the HCV type 5 sequences of the present invention as shown in Fig. 2;
- A256, P1631, V1677, Q1704, E1730, V1732, Q1741 and T1751 which are specific for the HCV type 3 and 5 sequences of the present invention as shown in Fig. 5 and 7;
- T71, A157, I227, T237, T240, Y250, V251, S260, M271, T2673, T2722, I2748 which are specific for the HCV type 3 and 4 sequences of the present invention as shown in Fig. 5 and 2,
- V192, Y194, A197, P249, S250, R294 which are specific for the HCV type 4 and 5 sequences of the present invention as shown in Fig. 5;
- I293 which is specific for the HCV type 4 and subtype 2d sequence of the present invention as shown in Fig. 5;
- D217 and R294 which are specific for the HCV type 3, 4 and 5 sequences of the present invention as shown in Fig. 5;
- L192 which is specific for the HCV type 3 and subtype 2d sequences of the present invention as shown in Fig. 5;
- G191 and T197 which are specific for the HCV type 3, 4 and subtype 2d sequences of the present invention as shown in Fig. 5;
- K232 which is specific for the HCV subtype 2d en type 5 sequences of the present invention as shown in Fig. 5.

and with said notation being composed of a letter, unambiguously representing the amino acid by its one-letter code, and a number representing the amino acid numbering according to Kato et al., 1990 (see also Table 1 for comparison with other isolates), as well as Figure 2 (NS

region), Figure 5 (Core/E1 region), Figure 7 (NS3/NS4 region), Figure 12 (E1/E2 region). Some of the above-mentioned amino acids may be contained in type or subtype specific epitopes.

For example M231 (detected in type 5) refers to a methionine at position 231. A glutamine (Q) is present at the same position 231 in type 3 isolates, whereas this position is occupied by an arginine in type 1 isolates and by a lysine (K) or asparagine (N) in type 2 isolates (see Figure 5).

The peptide or polypeptide according to this embodiment of the invention may be possibly labelled, or attached to a solid substrate, or coupled to a carrier molecule such as biotin, or mixed with a proper adjuvant.

The variable region in the core protein (V-CORE in Fig. 5) has been shown to be useful for serotyping (Machida et al., 1992). The sequence of the disclosed type 5 sequence in this region shows type-specific features. The peptide from amino acid 70 to 78 shows the following unique sequence for the sequences of the present invention (see figure 5):

QPTGRSWGQ (SEQ ID NO 93)

RSEGRSWAQ (SEQ ID NO 220)

and RTEGRSWAQ (SEQ ID NO 221)

Another preferred V-Core spanning region is the peptide spanning positions 60 to 78 of subtype 3c with sequence:

SRRQPIPRARRTEGRSWAQ (SEQ ID NO 268)

Five type-specific variable regions (V1 to V5) can be identified after aligning E1 amino acid sequences of the 4 genotypes, as shown in Figure 5.

Region V1 encompasses amino acids 192 to 203, this is the amino-terminal 10 amino acids of the E1 protein. The following unique sequences as shown in Fig. 5 can be deduced:

LEWRNTSGLYVL (SEQ ID NO 83)

VNYRNASGIYHI (SEQ ID NO 126)

QHYRNISGIYHV (SEQ ID NO 127)

EHYRNASGIYHI (SEQ ID NO 128)

IHYRNASGIYHI (SEQ ID NO 224)

VPYRNASGIYHV (SEQ ID NO 84)

VNYRNASGIYHI (SEQ ID NO 225)

VNYRNASGVYHI (SEQ ID NO 226)

VNYHNTSGIYHL (SEQ ID NO 227)

QHYNASGIYHV (SEQ ID NO 228)

QHYNVSGIYHV (SEQ ID NO 229)

IHYRNASDGYI (SEQ ID NO 230)

LQVKNTSSSYMV (SEQ ID NO 231)

Region V2 encompasses amino acids 213 to 223. The following unique sequences can be found in the V2 region as shown in Figure 5:

VYEADDVILHT (SEQ ID NO 85)

VYETEHILHL (SEQ ID NO 129)

VYEADHHIMHL (SEQ ID NO 130)

VYETDHILHL (SEQ ID NO 131)

VYEADNLILHA (SEQ ID NO 86)

VWQLRAIVLHV (SEQ ID NO 232)

VYEADYHILHL (SEQ ID NO 233)

VYETDNHILHL (SEQ ID NO 234)

VYETENHILHL (SEQ ID NO 235)

VFETVHHILHL (SEQ ID NO 236)

VFETEHILHL (SEQ ID NO 237)

VFETDHHIMHL (SEQ ID NO 238)

VYETENHILHL (SEQ ID NO 239)

VYEADALILHA (SEQ ID NO 240)

Region V3 encompasses the amino acids 230 to 242. The following unique V3 region sequences can be deduced from Figure 5:

VQDGNTSTCWTPV (SEQ ID NO 87)

VQDGNTSACWTPV (SEQ ID NO 241)

VRVGNSRCWVAL (SEQ ID NO 132)

VRTGNTSRCWVPL (SEQ ID NO 133)

VRAGNVSRCWTPV (SEQ ID NO 134)

EEKGNISRCWIPV (SEQ ID NO 242)

VKTGNQSRCWVAL (SEQ ID NO 243)

VRTGNQSRCWVAL (SEQ ID NO 244)

VKTGNQSRCWIAL (SEQ ID NO 245)

VKTGNVSRWIPL (SEQ ID NO 247)

VKTGNVSRWISL (SEQ ID NO 248)

VRKDNVSRWCWQI (SEQ ID NO 249)

Region V4 encompasses the amino acids 248 to 257. The following unique V4 region sequences can be deduced from figure 5:

VRYVGATTAS (SEQ ID NO 89)

APYIGAPLES (SEQ ID NO 135)

APYVGAPLES (SEQ ID NO 136)

AVSMDAPLES (SEQ ID NO 137)

APSLGAVTAP (SEQ ID NO 90)

APSPGAVTAP (SEQ ID NO 250)

VSQPGALTKG (SEQ ID NO 251)

VKYVGATTAS (SEQ ID NO 252)

APYIGAPVES (SEQ ID NO 253)

AQHLNAPLES (SEQ ID NO 254)

SPYVGAPLEP (SEQ ID NO 255)

SPYAGAPLEP (SEQ ID NO 256)

APYLGAPLEP (SEQ ID NO 257)

APYLGAPLES (SEQ ID NO 258)

APYVGAPLES (SEQ ID NO 259)

VPYLGAPLTS (SEQ ID NO 260)

APHLRAPLSS (SEQ ID NO 261)

APYLGAPLTS (SEQ ID NO 262)

Region V5 encompasses the amino acids 294 to 303. The following unique V5 region peptides can be deduced from figure 5:

RPRRHQTVQT (SEQ ID NO 91)

QPRRHWTQD (SEQ ID NO 138)

RPRRHWTQD (SEQ ID NO 139)

RPRQHATVQN (SEQ ID NO 92)

RPRQHATVQD (SEQ ID NO 263)

SPQHHKFVQD (SEQ ID NO 264)

RPRRLWTTQE (SEQ ID NO 265)

PPRIHETTQD (SEQ ID NO 266)

The variable region in the E2 region (HVR-2) of type 5a as shown in Figure 12 spanning amino acid positions 471 to 484 is also a preferred peptide according to the present invention

with the following sequence:

TISYANGSGPSDDK (SEQ ID NO 267)

The above given list of peptides are particularly suitable for vaccine and diagnostic development.

Also comprised in the present invention is any synthetic peptide or polypeptide containing at least 5 contiguous amino acids derived from the above-defined peptides in their peptidic chain.

According to a specific embodiment, the present invention relates to a composition as defined above, wherein said contiguous sequence is selected from any of the following HCV amino acid type 3 sequences:

- a sequence having a homology of more than 72%, preferably more than 74%, more preferably more than 77% and most preferably more than 80 or 84% homology to any of the amino acid sequences as represented in SEQ ID NO 14, 16, 18, 20, 22, 24, 26 or 28 (HD10, BR36, BR33 sequences) in the region spanning positions 140 to 319 in the Core/E1 region as shown in Figure 5;
- a sequence having a homology of more than 70%, preferably more than 72%, more preferably more than 75% homology, most preferably more than 81% homology to any of the amino acid sequences as represented in SEQ ID NO 14, 16, 18, 20, 22, 24, 26 or 28 (HD10, BR36, BR33 sequences) in the E1 region spanning positions 192 to 319 as shown in Figure 5;
- a sequence having a homology of more than 86%, preferably more than 88%, and most preferably more than 90% homology to the amino acid sequences as represented in SEQ ID NO 148 (type 3c); BE98 in the region spanning positions 1 to 110 in the Core region as shown in Figure 5;
- a sequence having a homology of more than 76%, preferably more than 78%, most preferably more than 80% to any of the amino acid sequences as represented in SEQ ID NO 30, 32, 34, 36, 38 or 40 (HCCI53, HD10, BR36 sequences) in the region spanning positions 1646 to 1764 in the NS3/NS4 region as shown in Figure 7 and 11;
- a sequence having a homology of more than 81%, preferably more than 83%, and most preferably more than 86% homology to any of the amino acid sequences as represented in SEQ ID NO 14, 16, 18, 20, 22, 24, 26 or 28 (HD10, BR36, BR33 sequences) in the region spanning positions 140 to 319 in the Core/E1 region as shown in Figure 5;
- a sequence having a homology of more than 81.5%, preferably more than 83%, and most

preferably more than 86% homology to any of the amino acid sequences as represented in SEQ ID NO 14, 16, 18, 20, 22, 24, 26 or 28 (HD10, BR36, BR33 sequences) in the E1 region spanning positions 192 to 319 as shown in Figure 5;

- a sequence having a homology of more than 86%, preferably more than 88%, most preferably more than 90% to the amino acid sequence as represented in SEQ ID NO 150; (type 3c BE98) in the region spanning positions 2645 to 2757 in the NS5B region as shown in Figure 2.

According to yet another embodiment, the present invention relates to a composition as defined above, wherein said contiguous sequence is selected from any of the following HCV amino acid type 4 sequences:

- a sequence having a homology of more than 80%, preferably more than 82%, most preferably more than 84% homology to any of the amino acid sequences as represented in SEQ ID NO 118, 120, and 122 (GB358, GB549, GB809 sequences) in the region spanning positions 127 to 319 of the Core/E1 region as shown in Figure 5;
- a sequence having a homology of more than 73%, preferably more than 75%, most preferably more than 78% homology in the E1 region spanning positions 192 to 319 to any of the amino acid sequences as represented in SEQ ID NO 118, 120, and 122 (GB358, GB549, GB809 sequences) in the region spanning positions 140 to 319 of the Core/E1 region as shown in Figure 5;
- a sequence having more than 85%, preferably more than 86%, most preferably more than 87% homology to any of the amino acid sequences as represented in SEQ ID NO 118, 120 or 122 (GB358, GB549, GB809 sequences) in the region spanning positions 192 to 319 of E1 as shown in Figure 5;
- a sequence showing more than 73%, preferably more than 74%, most preferably more than 75% homology to any of the amino acid sequences as represented in SEQ ID NO 106, 108, 110, 112, 114 or 116 (GB48, GB116, GB215, GB358, GB549, GB809 sequences) in the region spanning positions 2645 to 2757 of the NS5B region as shown in Figure 2;
- a sequence having any of the sequences as represented in SEQ ID NO 164 or 166 (GB809 and CAM600 sequences) in the Core/E1 region as shown in Figure 5;
- a sequence having any of the sequences as represented in SEQ ID NO 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188 or 190 (CAM600, GB809, CAMG22, CAMG27, GB549, GB438, CAR4/1205, CAR4/901, GB116, GB215, GB958, GB809-4 sequences) in the E1 region as shown in Figure 5;

- a sequence having any of the sequences as represented in SEQ ID NO 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212 (GB358, GB724, BE100, PC, CAM600, CAMG22, etc.) in the NS5B region.

The above-mentioned type 4 peptides polypeptides comprise at least an amino acid sequence selected from any HCV type 4 polyprotein with the exception of core sequence as disclosed by Simmonds et al. (1993, EG-29, see Figure 5).

According to yet another aspect, the present invention relates to a composition as defined above, wherein said contiguous sequence is selected from any of the following HCV amino acid type 5 sequences:

- a sequence having more than 93%, preferably more than 94%, most preferably more than 95% homology in the region spanning Core positions 1 to 191 to any of the amino acid sequences as represented in SEQ ID NO 42, 44, 46, 48, 50, 52 or 54 (PC sequences) and SEQ ID NO 152 (BE95) as shown in Figure 5;
- a sequence having more than 73%, preferably more than 74%, most preferably more than 76% homology in the region spanning E1 positions 192 to 319 to any of the amino acid sequences as represented in SEQ ID NO 42, 44, 46, 48, 50, 52 or 54 (PC sequences) as shown in Figure 5 ;
- a sequence having a more than 78%, preferably more than 80%, most preferably more than 83% homology to any of the amino acid sequences as represented in SEQ ID NO 42, 44, 46, 48, 50, 52, 54, 154, 156 (BE95, BE100) (PC sequences) in the region spanning positions 1 to 319 of the Core/E1 region as shown in Figure 5;
- a sequence having more than 90%, preferably more than 91%, most preferably more than 92% homology to any of the amino acid sequences represented in SEQ ID NO 56 to 58 (PC sequences) in the region spanning positions 1286 to 1403 of the NS3 region as shown in Figure 7 or 11;
- a sequence having more than 66%, more particularly 68%, most particularly 70% or more homology to any of the amino acid sequences as represented in SEQ ID NO 60 or 62 (PC sequences) in the region spanning positions 1646 to 1764 of the NS3/4 region as shown in Figure 7 or 11.

According to yet another embodiment, the present invention relates to a composition as defined above, wherein said contiguous sequence is selected from any of the following HCV amino acid type 2d sequences:

- a sequence having more than 83%, preferably more than 85%, most preferably more than

87% homology to the amino acid sequence as represented in SEQ ID NO 144 (NE92) in the region spanning positions 1 to 319 of the Core/E1 region as shown in Figure 5;

- a sequence having more than 79%, preferably more than 81%, most preferably more than 84% homology in the region spanning E1 positions 192 to 319 to the amino acid sequence as represented in SEQ ID NO 144 (NE92) as shown in Figure 12;
- a sequence having more than 95%, more particularly 96%, most particularly 97% or more homology to the amino acid sequence as represented in SEQ ID NO 146 (NE92) in the region spanning positions 2645 to 2757 of the NSSB region as shown in Figure 2.

The present invention also relates to a recombinant vector, particularly for cloning and/or expression, with said recombinant vector comprising a vector sequence, an appropriate prokaryotic, eukaryotic or viral promoter sequence followed by the nucleotide sequences as defined above, with said recombinant vector allowing the expression of any one of the HCV type 2 and/or HCV type 3 and/or type 4 and/or type 5 derived polypeptides as defined above in a prokaryotic, or eukaryotic host or in living mammals when injected as naked DNA, and more particularly a recombinant vector allowing the expression of any of the following HCV type 2d, type 3, type 4 or type 5 polypeptides spanning the following amino acid positions:

- a polypeptide starting at position 1 and ending at any position in the region between positions 70 and 326, more particularly a polypeptide spanning positions 1 to 70, 1 to 85, positions 1 to 120, positions 1 to 150, positions 1 to 191, positions 1 to 200, for expression of the Core protein, and a polypeptide spanning positions 1 to 263, positions 1 to 326, for expression of the Core and E1 protein;
- a polypeptide starting at any position in the region between positions 117 and 192, and ending at any position in the region between positions 263 and 326, for expression of E1, or forms that have the putative membrane anchor deleted (positions 264 to 293 plus or minus 8 amino acids);
- a polypeptide starting at any position in the region between positions 1556 and 1688, and ending at any position in the region between positions 1739 and 1764, for expression of the NS4 regions, more particularly a polypeptide starting at position 1658 and ending at position 1711 for expression of the NS4a antigen, and more particularly, a polypeptide starting at position 1712 and ending between positions 1743 and 1972, for example 1712-1743, 1712-1764, 1712-1782, 1712-1972, 1712 to 1782 and 1902 to 1972 for expression of the NS4b protein or parts thereof.

The term "vector" may comprise a plasmid, a cosmid, a phage, or a virus.

In order to carry out the expression of the polypeptides of the invention in bacteria such as *E. coli* or in eukaryotic cells such as in *S. cerevisiae*, or in cultured vertebrate or invertebrate hosts such as insect cells, Chinese Hamster Ovary (CHO), COS, BHK, and MDCK cells, the following steps are carried out:

- transformation of an appropriate cellular host with a recombinant vector, in which a nucleotide sequence coding for one of the polypeptides of the invention has been inserted under the control of the appropriate regulatory elements, particularly a promoter recognized by the polymerases of the cellular host and, in the case of a prokaryotic host, an appropriate ribosome binding site (RBS), enabling the expression in said cellular host of said nucleotide sequence. In the case of an eukaryotic host any artificial signal sequence or pre/pro sequence might be provided, or the natural HCV signal sequence might be employed, e.g. for expression of E1 the signal sequence starting between amino acid positions 117 and 170 and ending at amino acid position 191 can be used, for expression of NS4, the signal sequence starting between amino acid positions 1646 and 1659 can be used,
- culture of said transformed cellular host under conditions enabling the expression of said insert.

The present invention also relates to a composition as defined above, wherein said polypeptide is a recombinant polypeptide expressed by means of an expression vector as defined above.

The present invention also relates to a composition as defined above, for use in a method for immunizing a mammal, preferably humans, against HCV comprising administering a sufficient amount of the composition possibly accompanied by pharmaceutically acceptable adjuvants, to produce an immune response, more particularly a vaccine composition including HCV type 3 polypeptides derived from the Core, E1 or the NS4 region and/or HCV type 4 and/or HCV type 5 polypeptides and/or HCV type 2d polypeptides.

The present invention also relates to an antibody raised upon immunization with a composition as defined above by means of a process as defined above, with said antibody being reactive with any of the polypeptides as defined above, and with said antibody being preferably a monoclonal antibody.

The monoclonal antibodies of the invention can be produced by any hybridoma liable to be formed according to classical methods from splenic cells of an animal, particularly from

a mouse or rat, immunized against the HCV polypeptides according to the invention, or muteins thereof, or fragments thereof as defined above on the one hand, and of cells of a myeloma cell line on the other hand, and to be selected by the ability of the hybridoma to produce the monoclonal antibodies recognizing the polypeptides which has been initially used for the immunization of the animals.

The antibodies involved in the invention can be labelled by an appropriate label of the enzymatic, fluorescent, or radioactive type.

The monoclonal antibodies according to this preferred embodiment of the invention may be humanized versions of mouse monoclonal antibodies made by means of recombinant DNA technology, departing from parts of mouse and/or human genomic DNA sequences coding for H and L chains or from cDNA clones coding for H and L chains.

Alternatively the monoclonal antibodies according to this preferred embodiment of the invention may be human monoclonal antibodies. These antibodies according to the present embodiment of the invention can also be derived from human peripheral blood lymphocytes of patients infected with type 3, type 4 or type 5 HCV, or vaccinated against HCV. Such human monoclonal antibodies are prepared, for instance, by means of human peripheral blood lymphocytes (PBL) repopulation of severe combined immune deficiency (SCID) mice (for recent review, see Duchosal et al. 1992).

The invention also relates to the use of the proteins of the invention, muteins thereof, or peptides derived therefrom for the selection of recombinant antibodies by the process of repertoire cloning (Persson et al., 1991).

Antibodies directed to peptides derived from a certain genotype may be used either for the detection of such HCV genotypes, or as therapeutic agents.

The present invention also relates to the use of a composition as defined above for incorporation into an immunoassay for detecting HCV, present in biological sample liable to contain it, comprising at least the following steps:

- (i) contacting the biological sample to be analyzed for the presence of HCV antibodies with any of the compositions as defined above preferably in an immobilized form under appropriate conditions which allow the formation of an immune complex, wherein said polypeptide can be a biotinylated polypeptide which is covalently bound to a solid substrate by means of streptavidin or avidin complexes,
- (ii) removing unbound components,
- (iii) incubating the immune complexes formed with heterologous antibodies, which

specifically bind to the antibodies present in the sample to be analyzed, with said heterologous antibodies having conjugated to a detectable label under appropriate conditions,

- (iv) detecting the presence of said immunocomplexes visually or by means of densitometry and inferring the HCV serotype present from the observed hybridization pattern.

The present invention also relates to the use of a composition as defined above, for incorporation into a serotyping assay for detecting one or more serological types of HCV present in a biological sample liable to contain it, more particularly for detecting E1 and NS4 antigens or antibodies of the different types to be detected combined in one assay format, comprising at least the following steps:

- (i) contacting the biological sample to be analyzed for the presence of HCV antibodies or antigens of one or more serological types, with at least one of the compositions as defined above, an immobilized form under appropriate conditions which allow the formation of an immunocomplex,
- (ii) removing unbound components,
- (iii) incubating the immunocomplexes formed with heterologous antibodies, which specifically bind to the antibodies present in the sample to be analyzed, with said heterologous antibodies having conjugated to a detectable label under appropriate conditions,
- (iv) detecting the presence of said immunocomplexes visually or by means of densitometry and inferring the presence of one or more HCV serological types present from the observed binding pattern.

The present invention also relates to the use of a composition as defined above, for immobilization on a solid substrate and incorporation into a reversed phase hybridization assay, preferably for immobilization as parallel lines onto a solid support such as a membrane strip, for determining the presence or the genotype of HCV according to a method as defined above.

The present invention thus also relates to a kit for determining the presence of HCV genotypes as defined above present in a biological sample liable to contain them, comprising:

- possibly at least one primer composition containing any primer selected from those defined above or any other HCV type 3 and/or HCV type 4, and/or HCV type 5, or universal HCV primers,

- at least one probe composition as defined above, with said probes being preferentially immobilized on a solid substrate, and more preferentially on one and the same membrane strip,
- a buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the possibly amplified products to be carried out,
- means for detecting the hybrids resulting from the preceding hybridization,
- possibly also including an automated scanning and interpretation device for inferring the HCV genotypes present in the sample from the observed hybridization pattern.

The genotype may also be detected by means of a type-specific antibody as defined above, which is linked to any polynucleotide sequence that can afterwards be amplified by PCR to detect the immune complex formed (Immuno-PCR, Sano et al., 1992);

The present invention also relates to a kit for determining the presence of HCV antibodies as defined above present in a biological sample liable to contain them, comprising:

- at least one polypeptide composition as defined above, preferentially in combination with other polypeptides or peptides from HCV type 1, HCV type 2 or other types of HCV, with said polypeptides being preferentially immobilized on a solid substrate, and more preferentially on one and the same membrane strip,
- a buffer or components necessary for producing the buffer enabling binding reaction between these polypeptides and the antibodies against HCV present in the biological sample,
- means for detecting the immunocomplexes formed in the preceding binding reaction,
- possibly also including an automated scanning and interpretation device for inferring the HCV genotypes present in the sample from the observed binding pattern.

Figure Legends

Figure 1

Alignment of consensus nucleotide sequences for each of the type 3a isolates BR34, BR36, and BR33, deduced from the clones with SEQ ID NO 1, 5, 9; type 4 isolates GB48, GB116, GB215, GB358, GB549, GB809, CAM600, CAMG22, GB438, CAR4/1205, CAR1/501 (SEQ ID NO. 106, 108, 110, 112, 114, 116, 201, 203, 205, 207, 209 and 211); type 5a isolates BE95 and BE96 (SEQ ID NO 159 and 161) and type 2d isolate NE92 (SEQ ID NO 145) from the region between nucleotides 7932 and 8271, with known sequences from the corresponding region of isolates HCV-1, HCV-J, HC-J6, HC-J8, T1 and T9, and others as shown in Table 3.

Figure 2

Alignment of amino acids sequences deduced from the nucleic acid sequences as represented in Figure 1 from the subtype 3a clones BR34 (SEQ ID NO 2, 4), BR36 (SEQ ID NO 6, 8) and BR33 (SEQ ID NO 10, 12), the subtype 3c clone BE98 (SEQ ID NO 150), and the type 4 clones GB48 (SEQ ID NO 107), GB116 (SEQ ID NO 109), GB215 (SEQ ID NO 111), GB358 (SEQ ID NO 113), GB549 (SEQ ID NO 115) GB809 (SEQ ID NO 117); CAM600, CAMG22, GB438, CAR4/1205, CAR1/501 (SEQ ID NO 202, 204, 206, 208, 210, 212); the type 5a clones BE95 and BE96 (SEQ ID NO 160 and 162); as well as the subtype 2d isolate NE92 (SEQ ID NO 146) from the region between amino acids 2645 to 2757 with known sequences from the corresponding region of isolates HCV-I, HCV-J, HC-J6, and HC-J8, T1 and T9, and other sequences as shown in Table 3.

Figure 3

Alignment of type 2d, 3c, 4 and 5a nucleotide sequences from isolates NE92, BE98, GB358, GB809, CAM600, GB724, BE95 (SEQ ID NO 143, 147, 191, 163, 165, 193 and 151) in the Core region between nucleotide positions 1 and 500, with known sequences from the corresponding region of type 1, type 2, type 3 and type 4 sequences.

Figure 4

Alignment of nucleotide sequences for the subtype 2d isolate NE92 (SEQ ID NO 143), the type 4 isolates GB358 (SEQ ID NO 118 and 187), GB549 (SEQ ID NO 120 and 175), and

GB809-2 (SEQ ID NO 122 and 169), GB 809-4, BG116, GB215, CAM600, CAMG22, CAMG27, GB438, CAR4/1205, CAR4/901 (SEQ ID NO 189, 183, 185, 167, 171, 173, 177, 179, 181), sequences for each of the subtype 3a isolates HD10, BR36, and BR33, (SEQ ID NO 13, 15, 17 (HD10), 19, 21 (BR36) and 23, 25 or 27 (BR23) and the subtype 5a isolates BE95 and BE100 (SEQ ID NO 143 and 195) from the region between nucleotides 379 and 957, with known sequences from the corresponding region of type 1 and 2 and 3.

Figure 5

Alignment of amino acid sequences deduced from the new HCV nucleotide sequences of the Core/E1 region of isolates BR33, BR36, HD10, GB358, GB549, and GB809, PC or BE95, CAM600, and GB724 (SEQ ID NO. 14, 20, 24, 119 or 192, 121, 123 or 164, 54 or 152, 166 and 194) from the region between positions 1 and 319, with known sequences from type 1a (HCV-1), type 1b (HCV-J), type 2a (HC-JG), type 2b (HC-J8), NZL1, HCV-TR, positions 7-89 of type 3a (E-b1), and positions 8-88 of type 4a (EG-29). V-Core, variable region with type-specific features in the core protein, V1, variable region 1 of the E1 protein, V2, variable region 2 of the E1 protein, V3, variable region 3 of the E1 protein, V4, variable region 4 of the E1 protein, V5, variable region 5 of the E1 protein.

Figure 6

Alignment of nucleotide sequences of isolates HCCL53, HD10 and BR36, deduced from clones with SEQ ID NO 29, 31, 33, 35, 37 and 39, from the NS3/4 region between nucleotides 4664 to 5292, with known sequences from the corresponding region of isolates HCV-1, HCV-J, HC-J6, and HC-J8, EB1, EB2, EB6 and EB7.

Figure 7

Alignment of amino acid sequences deduced from the new HCV nucleotide sequences of the NS3/NS4 region of isolate BR36 (SEQ ID NO 36, 38 and 40) and BE95 (SEQ ID NO 270). NS4-1, indicates the region that was synthesized as synthetic peptide 1 of the NS4 region, NS4-5, indicates the region that was synthesized as synthetic peptide 5 of the NS4 region; NS4-7, indicates the region that was synthesized as synthetic peptide 7 of the NS4 region.

Figure 8

Reactivity of the three LIPA-selected (Stuyver et al., 1993) type 3 sera on the Inno-LIA HCV Ab II assay (Innogenetics) (left), and on the NS4-LIA test. For the NS4-LIA test, NS4-1, NS4-5, and NS4-7 peptides were synthesized based on the type 1 (HCV-1), type 2 (HC-J6) and type 3 (BR36) prototype isolate sequences as shown in Table 4, and applied as parallel lines onto a membrane strip as indicated. 1, serum BR33, 2, serum HD10, 3, serum DKH.

Figure 9

Nucleotide sequences of Core/E1 clones obtained from the PCR fragments PC-2, PC-3, and PC-4, obtained from serum BE95 (PC-2-1 (SEQ ID NO 41), PC-2-6 (SEQ ID NO 43), PC-4-1 (SEQ ID NO 45), PC-4-6 (SEQ ID NO 47), PC-3-4 (SEQ ID NO 49), and PC-3-8 (SEQ ID NO 51)) of subtype 5a isolate BE95.

A consensus sequence is shown for the Core and E1 region of isolate BE95, presented as PC C/E1 with SEQ ID NO 53. Y, C or T, R, A or G, S, C or G.

Figure 10

Alignment of nucleotide sequences of clones with SEQ ID NO 197 and 199 (PC sequences, see also SEQ ID NO 55, 57, 59) and SEQ ID NO 35, 37 and 39 (BR36 sequences) from the NS3/4 region between nucleotides 3856 to 5292, with known sequences from the corresponding region of isolates HCV-1, HCV-J, HC-J6, and HC-J8.

Figure 11

Alignment of amino acid sequences of subtype 5a BE95 isolate PC clones with SEQ ID NO 56 and 58, from the NS3/4 region between amino acids 1286 to 1764, with known sequences from the corresponding region of isolates HCV-1, HCV-J, HC-J6, and HC-J8.

Figure 12

Alignment of amino acid sequences of subtype 5a isolate BE95 (SEQ ID NO 158) in the E1/E2 region spanning positions 328 to 546, with known sequences from the corresponding region of isolates HCV-1, HCV-J, HC-J6, HC-J8, NZL1 and HCV-TR (see Table 3).

Figure 13

Alignment of the nucleotide sequences of subtype 5a isolate BE95 (SEQ ID NO 157) in the E1/E2 region with known HCV sequences as shown in Table 3.

EXAMPLES

Example 1: The NS5b region of HCV type 3

Type 3 sera, selected by means of the INNO-LiPA HCV research kit (Stuyver et al., 1993) from a number of Brazilian blood donors, were positive in the HCV antibody ELISA (Innotest HCV Ab II; Innogenetics) and/or in the INNO-LiA HCV Ab II confirmation test (Innogenetics). Only those sera that were positive after the first round of PCR reactions (Stuyver et al., 1993) were retained for further study.

Reverse transcription and nested PCR: RNA was extracted from 50 μ l serum and subjected to cDNA synthesis as described (Stuyver et al., 1993). This cDNA was used as template for PCR, for which the total volume was increased to 50 μ l containing 10 pmoles of each primer, 3 μ l of 10x Pfu buffer 2 (Stratagene) and 2.5 U of Pfu DNA polymerase (Stratagene). The cDNA was amplified over 45 cycles consisting of 1 min 94°C, 1 min 50°C and 2 min 72°C. The amplified products were separated by electrophoresis, isolated, cloned and sequenced as described (Stuyver et al., 1993).

Type 3a and 3b-specific primers in the NS5 region were selected from the published sequences (Mori et al., 1992) as follows:

for type 3a:

HCPri161(+): 5'-ACCGGAGGCCAGGAGAGTGATCTCTCTCC-3' (SEQ ID NO 63) and

HCPri162(-): 5'-GGGCTGCTCTATCCTCATCGACGCCATC-3' (SEQ ID NO 64);

for type 3b:

HCPri163(+): 5'-GCCAGAGGCTCGGAAGGCGATCAGCGCT-3' (SEQ ID NO 65) and

HCPri164(-): 5'-GAGCTGCTCTGCTCCTCGACGCCGCA-3' (SEQ ID NO 66)

Using the Line Probe Assay (LiPA) (Stuyver et al., 1993), seven high-titer type 3 sera were selected and subsequently analyzed with the primer sets HCPri161/162 for type 3a, and HCPri163/164 for type 3b. None of these sera was positive with the type 3b primers. NS5 PCR fragments obtained using the type 3a primers from serum BR36 (BR36-23), serum BR33 (BR33-2) and serum BR34 (BR34-4) were selected for cloning. The following sequences were obtained from the PCR fragments:

From fragment BR34-4:

BR34-4-20 (SEQ ID NO 1), BR34-4-19 (SEQ ID NO 3)

From fragment BR36-23:

BR36-23-18 (SEQ ID NO 5), BR36-23-20 (SEQ ID NO 7)

From fragment BR33-2:

BR33-2-17 (SEQ ID NO 9), BR33-2-21 (SEQ ID NO 11)

An alignment of sequences with SEQ ID NO 1, 5 and 9 with known sequences is given in Figure 1. An alignment of the deduced amino acid sequences is shown in Figure 2. The 3 isolates are very closely related to each other (mutual homologies of about 95%) and to the published sequences of type 3a (Mori et al., 1992), but are only distantly related to type 1 and type 2 sequences (Table 5). Therefore, it is clearly demonstrated that NS5 sequences from LiPA-selected type 3 sera are indeed derived from a type 3 genome. Moreover, by analyzing the NS5 region of serum BR34, for which no 5'UR sequences were determined as described in Stuyver et al. (1993), the excellent correlation between typing by means of the LiPA and genotyping as deduced from nucleotide sequencing was further proven.

Example 2: The Core/E1 region of HCV type 3

After aligning the sequences of HCV-1 (Choo et al., 1991), HCV-J (Kato et al., 1990), HC-J6 (Okamoto et al., 1991), and HC-J8 (Okamoto et al., 1992), PCR primers were chosen in those regions of little sequence variation. Primers HCP23(+): 5'-CTCATGGGGTACATTCCGCT-3' (SEQ ID NO 67) and HCP54(-): 5'-TATTACCAGTTTCATCATCATATCCCA-3' (SEQ ID NO 68), were synthesized on a 392 DNA/RNA synthesizer (Applied Biosystems). This set of primers was selected to amplify the sequence from nucleotide 397 to 957 encoding amino acids 140 to 319 (Kato et al., 1990): 52 amino acids from the carboxyterminus of core and 128 amino acids of E1 (Kato et al., 1990). The amplification products BR36-9, BR33-1, and HD10-2 were cloned as described (Stuyver et al., 1993). The following clones were obtained from the PCR fragments:

From fragment HD10-2:

HD10-2-5 (SEQ ID NO 13), HD10-2-14 (SEQ ID NO 15), HD10-2-21 (SEQ ID NO 17)

From fragment BR36-9:

BR36-9-13 (SEQ ID NO 19), BR36-9-20 (SEQ ID NO 21),

From fragment BR33-1:

BR33-1-10 (SEQ ID NO 23), BR33-1-19 (SEQ ID NO 25), BR33-1-20 (SEQ ID NO 27),

An alignment of the type 3 E1 nucleotide sequences (HD10, BR36, BR33) with SEQ ID NO 13, 19 and 23 with known E1 sequences is presented in Figure 4. Four variations were detected in the E1 clones from serum HD10 and BR36, while only 2 were found in BR33. All are silent third letter variations, with the exception of mutations at position 40 (L to P)

and 125 (M to I). The homologies of the type 3 E1 region (without core) with type 1 and 2 prototype sequences are depicted in Table 5.

In total, 8 clones covering the core/E1 region of 3 different isolates were sequenced and the E1 portion was compared with the known genotypes (Table 3) as shown in Figure 5. After computer analysis of the deduced amino acid sequence, a signal-anchor sequence at the core carboxyterminus was detected which might, through analogy with type 1b (Hijikata et al., 1991), promote cleavage before the LEWRN sequence (position 192, Fig. 5). The L-to-P mutation in one of the HD10-2 clones resides in this signal-anchor region and potentially impairs recognition by signal peptidase (computer prediction). Since no examples of such substitutions were found at this position in previously described sequences, this mutation might have resulted from reverse transcriptase or *Pfu* polymerase misincorporation. The 4 amino-terminal potential N-linked glycosylation sites, which are also present in HCV types 1a and 2, remain conserved in type 3. The N-glycosylation site in type 1b (aa 250, Kato et al., 1990) remains a unique feature of this subtype. All E1 cysteines, and the putative transmembrane region (aa 264 to 293, computer prediction) containing the aspartic acid at position 279, are conserved in all three HCV types. The following hypervariable regions can be delineated: V1 from aa 192 to 203 (numbering according to Kato et al., 1990), V2 (213-223), V3 (230-242), V4 (248-257), and V5 (294-303). Such hydrophilic regions are thought to be exposed to the host defense mechanisms. This variability might therefore have been induced by the host's immune response. Additional putative N-linked glycosylation sites in the V4 region in all type 1b isolates known today and in the V5 region of HC-J8 (type 2b) possibly further contribute to modulation of the immune response. Therefore, analysis of this region, in the present invention, for type 3 and 4 sequences has been instrumental in the delineation of epitopes that reside in the V-regions of E1, which will be critical for future vaccine and diagnostics development.

Example 3: The NS3/NS4 region of HCV Type 3

For the NS3/NS4 border region, the following sets of primers were selected in the regions of little sequence variability after aligning the sequences of HCV-1 (Choo et al., 1991), HCV-J (Kato et al., 1990), HC-J6 (Okamoto et al., 1991), and HC-J8 (Okamoto et al., 1992) (smaller case lettering is used for nucleotides added for cloning purposes):

set A:

HCP116(+): 5'-tttAAATACATCATGRCITGYATG-3' (SEQ ID NO 69)

HCP66 (-): 5'-ctattaTTGTATCCCRCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

set B:

HCP116(+): 5'-ttttAAATACATCATGRCITGYATG-3' (SEQ ID NO 69)

HCP118(-): 5'-actagtcgactaYTGATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO 71)

set C:

HCP117(+): 5'-ttttAAATACATCGCIRCITGCATGCA-3' (SEQ ID NO 72)

HCP66 (-): 5'-ctattaTTGTATCCCRCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

set D:

HCP117(+): 5'-ttttAAATACATCGCIRCITGCATGCA-3' (SEQ ID NO 72)

HCP118(-): 5'-actagtcgactaYTGATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO 71)

set E:

HCP116(+): 5'-ttttAAATACATCATGRCITGYATG-3' (SEQ ID NO 69)

HCP119(-): actagtcgactaRTTIGCIATAGCCG/TRTTCATCCA YTG-3' (SEQ ID NO 73)

set F:

HCP117(+): 5'-ttttAAATACATCGCIRCITGCATGCA-3' (SEQ ID NO 72)

HCP119(-): actagtcgactaRTTIGCIATAGCCG/TRTTCATCCA YTG-3' (SEQ ID NO 73)

set G:

HCP131(+): 5'-ggaattctagaCCITCITGGGAYGARAYITGGAARTG-3' (SEQ ID NO 74)

HCP66 (-): 5'-ctattaTTGTATCCCRCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

set H:

HCP130(+): 5'-ggaattctagACIGCITAYCARGCIACIGTITGYGC-3' (SEQ ID NO 75)

HCP66 (-): 5'-ctattaTTGTATCCCRCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

set I:

HCP134(+): 5'-CATATAGATGCCCACTTCCTATC-3' (SEQ ID NO 76)

HCP66 (-): 5'-ctattaTTGTATCCCRCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

set J:

HCP131(+): 5'-ggaattctagaCCITCITGGGAYGARAYITGGAARTG-3' (SEQ ID NO 74)

HCP118(-): 5'-actagtcgactaYTGATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO

71)

set K:

HCP130(+): 5'-ggaattctagACIGCITAYCARGCIACIGTITGYGC-3' (SEQ ID NO 75)

HCP118(-): 5'-actagtcgactaYTGATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO

71)

set L:

HCP134(+): 5'-CATATAGATGCCCACTTCCTATC-3' (SEQ ID NO 76)

HCP118(-): 5'-actagtcgactaYTGATICCRCTIATRWARTCCACAT-3' (SEQ ID NO 71)

set M:

HCP3(+): 5'-GTGTGCCAGGACCATC-3' (SEQ ID NO 77) and

HCP4(-): 5'-GACATGCATGTCATGATGTA-3 (SEQ ID NO 78)

set N:

HCP3(+): 5'-GTGTGCCAGGACCATC-3' (SEQ ID NO 77) and

HCP118(-): 5'-actagtcgactaYTGATICCRCTIATRWARTCCACAT-3' (SEQ ID NO 71)

set O:

HCP3(+): 5'-GTGTGCCAGGACCATC-3' (SEQ ID NO 77) and

HCP66 (-): 5'-ctattaTTGTATCCCRCCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

No PCR products could be obtained with the sets of primers A, B, C, D, E, F, G, H, I, J, K, L, M, and N, on random-primed cDNA obtained from type 3 sera. With the primer set O, no fragment could be amplified from type 3 sera. However, a smear containing a few weakly stainable bands was obtained from serum BR36. After sequence analysis of several DNA fragments, purified and cloned from the area around 300 bp on the agarose gel, only one clone, HCC153 (SEQ ID NO 29), was shown to contain HCV information. This sequence was used to design primer HCP152.

A new primer set P was subsequently tested on several sera.

set P:

HCP152(+): 5'-TACGCCTCTTCTATATCGGTTGGGGCCTG-3' (SEQ ID NO 79) and

HCP66(-): 5'-CTATTATTGTATCCCRCCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

The 464-bp HCP152/66 fragment was obtained from serum BR36 (BR36-20) and serum HD10 (HD10-1). The following clones were obtained from these PCR products:

From fragment HD10-1:

HD10-1-25 (SEQ ID NO 31), HD10-1-3 (SEQ ID NO 33),

From fragment BR36-20:

BR36-20-164 (SEQ ID NO 35), BR36-20-165 (SEQ ID NO 37), BR36-20-166 (SEQ ID NO 39),

The nucleotide sequences obtained from clones with SEQ ID NO 29, 31, 33, 35, 37 or 39 are shown aligned with the sequences of prototype isolates of other types of HCV in Figure 6. In addition to one silent 3rd letter variation, one 2nd letter mutation resulted in an

E to G substitution at position 175 of the deduced amino acid sequence of BR36 (Fig. 7). Serum HD10 clones were completely identical. The two type 3 isolates were nearly 94% homologous in this NS4 region. The homologies with other types are presented in Table 5.

Example 4: Analysis of the anti-NS4 response to type-specific peptides

As the NS4 sequence contains the information for an important epitope cluster, and since antibodies towards this region seem to exhibit little cross-reactivity (Chan et al., 1991), it was worthwhile to investigate the type-specific antibody response to this region. For each of the 3 genotypes, HCV-1 (Choo et al., 1991), HC-J6 (Okamoto et al., 1991) and BR36 (present invention), three 20-mer peptides were synthesized covering the epitope region between amino acids 1688 and 1743 (as depicted in table 6). The synthetic peptides were applied as parallel lines onto membrane strips. Detection of anti-NS4 antibodies and color development was performed according to the procedure described for the INNO-LIA HCV Ab II kit (Innogenetics, Antwerp). Peptide synthesis was carried out on a 9050 PepSynthesizer (Millipore). After incubation with 15 LiPA-selected type 3 sera, 9 samples showed reactivity towards NS4 peptides of at least 2 different types, but a clearly positive reaction was observed for 3 sera (serum BR33, HD30 and DKH) on the type 3 peptides, while negative (serum BR33 and HD30) or indeterminate (serum DKH) on the type 1 and type 2 NS4 peptides; 3 sera tested negative for anti-NS4 antibodies (Figure 8). Using the same membrane strips coated with the 9 peptides as indicated above and as shown in Figure 8, 38 type 1 sera (10 type 1a and 28 type 1b), 11 type 2 sera (10 type 2a and 1 type 2b), 12 type 3a sera and 2 type 4 sera (as determined by the LiPA procedure) were also tested. As shown in Table 8, the sera reacted in a genotype-specific manner with the NS4 epitopes. These results demonstrate that type-specific anti-NS4 antibodies can be detected in the sera of some patients. Such genotype-specific synthetic peptides might be employed to develop serotyping assays, for example a mixture of the nine peptides as indicated above, or combined with the NS4 peptides from the HCV type 4 or 6 genotype or from new genotypes corresponding to the region between amino acids 1688 and 1743, or synthetic peptides of the NS4 region between amino acids 1688 and 1743 of at least one of the 6 genotypes, combined with the E1 protein or deletion mutants thereof, or synthetic E1 peptides of at least one of the genotypes. Such compositions could be further extended with type-specific peptides or proteins, including for example the region between amino acids 68 and 91 of the core protein, or more preferably the region between amino acids 68 and 78. Furthermore, such type-specific

antigens may be advantageously used to improve current diagnostic screening and confirmation assays and/or HCV vaccines.

Example 5 The Core and E1 regions of HCV type 5

Sample BE95 was selected from a group of sera that reacted positive in a prototype Line Probe Assay as described earlier (Stuyver et al., 1993), because a high-titer of HCV RNA could be detected, enabling cloning of fragments by a single round of PCR. As no sequences from any coding region of type 5 has been disclosed yet, synthetic oligonucleotides for PCR amplification were chosen in the regions of little sequence variation after aligning the sequences of HCV-1 (Choo et al., 1991), HCV-J (Kato et al., 1990), HC-J6 (Okamoto et al., 1991), HC-J8 (Okamoto et al., 1992), and the new type 3 sequences of the present invention HD10, BR33, and BR36 (see Figure 5, Example 2). The following sets of primers were synthesized on a 392 DNA/RNA synthesizer (Applied Biosystems):

Set 1:

HCPPr52(+): 5'-atgTTGGGTAAGGTCATCGATACCCT-3' (SEQ ID NO 80) and

HCPPr54(-): 5'-ctattaCCAGTTCATCATCATATCCCA-3' (SEQ ID NO 78)

Set 2:

HCPPr41(+): 5'-CCCGGGAGGTCTCGTAGACCGTGCA-3' (SEQ ID NO 81) and

HCPPr40(-): 5'-ctattaAAGATAGAGAAAGAGCAACCGGG-3' (SEQ ID NO 82)

Set 3:

HCPPr41(+): 5'-CCCGGGAGGTCTCGTAGACCGTGCA-3' (SEQ ID NO 81) and

HCPPr54(-): 5'-ccattaCCAGTTCATCATCATATCCCA-3' (SEQ ID NO 78)

The three sets of primers were employed to amplify the regions of the type 5 isolate PC as described (Stuyver et al., 1993). Set 1 was used to amplify the E1 region and yielded fragment PC-4, set 2 was designed to yield the Core region and yielded fragment PC-2. Set 3 was used to amplify the Core and E1 region and yielded fragment PC-3. These fragments were cloned as described (Stuyver et al., 1993). The following clones were obtained from the PCR fragments:

From fragment PC-2:

PC-2-1 (SEQ ID NO 41), PC-2-6 (SEQ ID NO 43),

From fragment PC-4:

PC-4-1 (SEQ ID NO 45), PC-4-6 (SEQ ID NO 47),

From fragment PC-3:

PC-3-4 (SEQ ID NO 49), PC-3-8 (SEQ ID NO 51)

An alignment of sequences with SEQ ID NO 41, 43, 45, 47, 49 and 51, is given in Figure 9. A consensus amino acid sequence (PC C/E1; SEQ ID NO 54) can be deduced from each of the 2 clones cloned from each of the three PCR fragments as depicted in Figure 5, which overlaps the region between nucleotides 1 and 957 (Kato et al., 1990). The 6 clones are very closely related to each other (mutual homologies of about 99.7%).

An alignment of nucleotide sequence with SEQ ID NO 53 or 151 (PC C/E1 from isolate BE95) with known nucleotide sequences from the Core/E1 region is given in Figure 3. The clone is only distantly related to type 1, type 2, type 3 and type 4 sequences (Table 5).

Example 6: NS3/NS4 region of HCV type 5

Attempts were undertaken to clone the NS3/NS4 region of the isolate BE95, described in example 5. The following sets of primers were selected in the regions of little sequence variability after aligning the sequences of HCV-1 (Choo et al., 1991), HCV-J (Kato et al., 1991), HC-J6 (Okamoto et al., 1991), and HC-J8 (Okamoto et al., 1992) and of the sequences obtained from type 3 sera of the present invention (SEQ ID NO 31, 33, 35, 37 and 39); smaller case lettering is used for nucleotides added for cloning purposes:

set A:

HCPrl16(+): 5'-ttttAAATACATCATGRCITGYATG-3' (SEQ ID NO 66)

HCPrl66 (-): 5'-ctattattGTATCCCRCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

set B:

HCPrl16(+): 5'-ttttAAATACATCATGRCITGYATG-3' (SEQ ID NO 69)

HCPrl18(-): 5'-actagtcgactaYTGIATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO 71)

set C:

HCPrl17(+): 5'-ttttAAATACATCGCIRCITGCATGCA-3' (SEQ ID NO 72)

HCPrl66 (-): 5'-ctattattGTATCCCRCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

set D:

HCPrl17(+): 5'-ttttAAATACATCGCIRCITGCATGCA-3' (SEQ ID NO 72)

HCPrl18(-): 5'-actagtcgactaYTGIATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO 71)

set E:

HCPrl16(+): 5'-ttttAAATACATCATGRCITGYATG-3' (SEQ ID NO 69)

HCPrl19(-): actagtcgactaRTTIGCIATAGCCG/TRITCATCCAYTG-3' (SEQ ID NO 73)

set F:

HCPrl17(+): 5'-ttttAAATACATCGCIRCITGCATGCA-3' (SEQ ID NO 72)

HCPrl19(-): actagtcgactaRTTIGCIATIAGCCG/TRITTCATCCAYTG-3' (SEQ ID NO 73)

set G:

HCPrl131(+): 5'-ggaattctagaCCITCITGGGAYGARAYITGGAARTG-3' (SEQ ID NO 74)

HCPrl66 (-): 5'-ctatttaTTGTATCCCRCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

set H:

HCPrl130(+): 5'-ggaattctagACIGCITAYCARGCIACIGTITGYGC-3' (SEQ ID NO 75)

HCPrl66 (-): 5'-ctatttaTTGTATCCCRCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

set I:

HCPrl134(+): 5'-CATATAGATGCCCCACTTCCTATC-3' (SEQ ID NO 76)

HCPrl66 (-): 5'-ctatttaTTGTATCCCRCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

set J:

HCPrl131(+): 5'-ggaattctagaCCITCITGGGAYGARAYITGGAARTG-3' (SEQ ID 74)

HCPrl118(-): 5'-actagtcgactaYTGIATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO 71)

set K:

HCPrl130(+): 5'-ggaattctagACIGCITAYCARGCIACIGTITGYGC-3' (SEQ ID NO 75)

HCPrl118(-): 5'-actagtcgactaYTGIATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO 71)

set L:

HCPrl134(+): 5'-CATATAGATGCCCCACTTCCTATC-3' (SEQ ID NO 76)

HCPrl118(-): 5'-actagtcgactaYTGIATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO 71)

set M:

HCPrl3(+): 5'-GTGTGCCAGGACCATC-3' (SEQ ID NO 77) and

HCPrl4(-): 5'-GACATGCATGTCATGATGTA-3' (SEQ ID NO 78)

set N:

HCPrl3(+): 5'-GTGTGCCAGGACCATC-3' (SEQ ID NO 77) and

HCPrl118(-): 5'-actagtcgactaYTGIATICCRCTIATRWARTTCCACAT-3' (SEQ ID NO

71)

set O:

HCPrl3(+): 5'-GTGTGCCAGGACCATC-3' (SEQ ID NO 77) and

HCPrl66 (-): 5'-ctatttaTTGTATCCCRCTGATGAARTTCCACAT-3' (SEQ ID NO 70)

No PCR products could be obtained with the sets of primers A, B, C, D, E, F, G, H, I, J, K, L, M, and N, on random-primed cDNA obtained from type 3 sera. However,

set O yielded what appeared to be a PCR artifact fragment estimated about 1450 base pairs, instead of the expected 628 base pairs. Although it is not expected that PCR artifact fragments contain information of the gene or genome that was targeted in the experiment, efforts were put in cloning of this artifact fragment, which was designated fragment PC-1. The following clones, were obtained from fragment PC-1:

PC-1-37 (SEQ ID NO 59 and SEQ ID NO 55), PC-1-48 (SEQ ID NO 61 and SEQ ID NO 57)

The sequences obtained from the 5' and 3' ends of the clones are given in SEQ ID NOS 55, 57, 59, and 61, and the complete sequences with SEQ ID NO 197 and 199 are shown aligned with the sequences of prototype isolates of other types of HCV in Figure 10 and the alignment of the deduced amino acid sequences is shown in Figure 11 and 7. Surprisingly, the PCR artifact clone contained HCV information. The positions of the sequences within the HCV genome are compatible with a contiguous HCV sequence of 1437 nucleotides, which was the estimated size of the cloned PCR artifact fragment. Primer HCPr66 primed correctly at the expected position in the HCV genome. Therefore, primer HCPr3 must have incidentally misprimed at a position 809 nucleotides upstream of its legitimate position in the HCV genome. This could not be expected since no sequence information was available from a coding region of type 5.

Example 7 : The E2 region of HCV type 5

Serum BE95 was chosen for experiments aimed at amplifying a part of the E2 region of HCV type 5.

After aligning the sequences of HCV-1 (2), HCV-J(1), HC-J6 (3), and HC-J8 (4), PCR primers were chosen in those regions of little sequence variation.

Primers HCPr109(+): 5'-TGGGATATGATGATGAACCTGGTC-3' (SEQ ID NO 141) and HCPr14(-): 5'-CCAGGTACAACCGAACCAATTGCC-3' (SEQ ID NO 142) were combined to amplify the aminoterminal region of the E2/NS1 region, and were synthesized on a 392 DNA/RNA synthesizer (Applied Biosystems). With primers HCPr109 and HCPr14, a PCR fragment of 661 bp was generated, containing 169 nucleotides corresponding to the E1 carboxyterminus and 492 bases from the region encoding the E2 aminotermus.

An alignment of the type 5 E1/E2 sequences with seq ID NO. 158 with known sequences is presented in Figure 10. The deduced protein sequence was compared with the different

genotypes (Fig. 12, amino acids 328-546). In the E1 region, there were no extra structural important motifs found. The aminoterminal part of E2 was hypervariable when compared with the other genotypes. All 6 N-glycosylation sites and all 7 cysteine residue's were conserved in this E2 region. To preserve alignment, it was necessary to introduce a gap between aa 474 and 475 as for type 3a, but not between aa 480 and 481, as for type 2.

Example 8 : The NS5b region of HCV type 4

Type 4 sera GB48, GB116, GB215, and GB358, selected by means of the line probe assay (LiPA, Stuyver et al., 1993), as well as sera GB549 and GB809 that could not be typed by means of this LiPA (only hybridization was observed with the universal probes), were selected from Gabonese patients. All these sera were positive after the first round of PCR reactions for the 5' untranslated region (Stuyver et al., 1993) and were retained for further study.

RNA was isolated from the sera and cDNA synthesized as described in example 1.

Universal primers in the NS5 region were selected after alignment of the published sequences as follows:

HCP206(+): 5'-TG GGGATCCCGTATGATACCCGCTGCTTTGA-3'

(SEQ ID NO. 124) and

HCP207(-): 5'-GGCGGAATTCCTGGTCATAGCCTCCGTGAA-3'

(SEQ ID NO. 125);

and were synthesized on a 392 DNA/RNA synthesizer (Applied Biosystems). Using the Line Probe Assay (LiPA), four high-titer type 4 sera and 2 sera that could not be classified were selected and subsequently analyzed with the primer set HCP206/207. NS5 PCR fragments obtained using these primers from serum GB48 (GB48-3), serum GB116 (GB116-3), serum GB215 (GB215-3), serum GB358 (GB358-3), serum GB549 (GB549-3), and serum GB809 (GB809-3), were selected for cloning. The following sequences were obtained from the PCR fragments:

From fragment GB48-3 : GB48-3-10 (SEQ ID NO. 106)

From fragment GB116-3: GB116-3-5 (SEQ ID NO. 108)

From fragment GB215-3: GB215-3-8 (SEQ ID NO. 110)

From fragment GB358-3: GB358-3-3 (SEQ ID NO. 112)

From fragment GB549-3: GB549-3-6 (SEQ ID NO. 114)

From fragment GB809-3: GB809-3-1 (SEQ ID NO. 116)

An alignment of nucleotide sequences with SEQ ID NO. 106, 108, 110, 112, 114, and 116 with known sequences is given in Figure 1. An alignment of deduced amino acid sequences with SEQ ID NO. 107, 109, 111, 113, 115, and 117 with known sequences is given in Figure 2. The 4 isolates that had been typed as type 4 by means of LiPA are very closely related to each other (mutual homologies of about 95%), but are only distantly related to type 1, type 2, and type 3 sequences (e.g. GB358 shows homologies of 65.6 to 67.7% with other genotypes, Table 4). The sequence obtained from sera GB549 and GB809 also show similar homologies with genotypes 1, 2, and 3 (65.9 to 68.8% for GB549 and 65.0 to 68.5% for GB809, Table 4), but an intermediate homology of 79.7 to 86.8% (often observed between subtypes of the same type) exists between GB549 or GB809 with the group of isolates consisting of GB48, GB116, GB215, and GB358, or between GB549 and GB809. These data indicate the discovery of 3 new subtypes within the HCV genotype 4: in the present invention, these 3 subtypes are designated subtype 4c, represented by isolates GB48, GB116, GB215, and GB358, subtype 4g, represented by isolate GB549, and subtype 4e, represented by isolate GB809. Although the homologies observed between subtypes in the NS5 region seem to indicate a closer relationship between subtypes 4c and 4e, the homologies observed in the E1 region indicate that subtypes 4g and 4e show the closest relation (see example 8).

Example 9 : The Core/E1 region of HCV type 4

From each of the 3 new type 4 subtypes, one representative serum was selected for cloning experiments in the Core/E1 region. GB549 (subtype 4g) and GB809 (subtype 4e) were analyzed together with isolate GB358 that was chosen from the subtype 4c group.

Synthetic oligonucleotides:

After aligning the sequences of HCV-1 (2), HCV-J(1), HC-J6 (3), and HC-J8 (4), PCR primers were chosen in those regions of little sequence variation.

Primers HCP_r52(+): 5'-atgTTGGGTAAGGTCATCGATACCT-3', HCP_r23(+): 5'-CTCATGGGGTACATTCCGCT-3', and HCP_r54(-): 5'-CTATTACCAGTTCATCATCATATCCCA-3', were synthesized on a 392 DNA/RNA synthesizer (Applied Biosystems). The sets of primers HCP_r23/54 and HCP_r52/54 were used, but only with the primer set HCP_r52/54, PCR fragments could be obtained. This set of primers amplified the sequence from nucleotide 379 to 957 encoding amino acids 127 to 319: 65 amino acids from the carboxyterminus of core and 128 amino acids of E1. The

amplification products GB358-4, GB549-4, and GB809-4 were cloned as described in example

1. The following clones were obtained from the PCR fragments:

From fragment GB358-4: GB358-4-1 (SEQ ID NO 118)

From fragment GB549-4: GB549-4-3 (SEQ ID NO 120)

From fragment GB809-4: GB809-4-3 (SEQ ID NO 122)

An alignment of the type 4 Core/E1 nucleotide sequences with seq ID NO. 118, 120, and 122 with known sequences is presented in Figure 4. The homologies of the type 4 E1 region (without core) with type 1, type 2, type 3, and type 5 prototype sequences are depicted in Table 4. Homologies of 53 to 66% are observed with representative isolates of non-type 4 genotypes. Observed homologies in the E1 region within type 4, between the different subtypes, ranges from 75.2 to 78.4%. The recently disclosed sequences of the core region of Egyptian type 4 isolates (for example EG-29 in Figure 3) described by Simmonds et al. (1993) do not allow alignment with the Gabonese sequences (as described in the present invention) in the NSB region and may belong to different type 4 subtypes(s) as can be deduced from the core sequences. The deduced amino acid sequences with SEQ ID NO 119, 121, and 123 are aligned with other prototype sequences in Figure 5. Again, type-specific variation mainly resides in the variable V regions, designated in the present invention, and therefore, type-4-specific amino acids or V regions will be instrumental in diagnosis and therapeutics for HCV type 4.

Example 10 : The Core/E1 and NS5b regions of new HCV type 2, 3 and 4 subtypes

Samples NE92 (subtype 2d), BE98 (subtype 3c), CAM600 and GB809 (subtype 4e), CAMG22 and CAMG27 (subtype 4f), GB438 (subtype 4h), CAR4/1205 subtype (4i), CAR1/501 (subtype 4j), CAR1/901 (subtype 4?), and GB724 (subtype 4?) were selected from a group of sera that reacted positive but aberrantly in a prototype Line Probe Assay as described earlier (Stuyver et al., 1993). Another type 5a isolate BE100 was also analyzed in the C/E1 region, and yet another type 5a isolate BE96 in the NS5b region. A high-titer of HCV RNA could be detected, enabling cloning of fragments by a single round of PCR. As no sequences from any coding region of these subtypes had been disclosed yet, synthetic oligonucleotides for PCR amplification were chosen in the regions of little sequence variation after aligning the sequences of HCV-1 (Choo et al., 1991), HCV-J (Kato et al., 1990), HC-J6 (Okamoto et al., 1991), HC-J8 (Okamoto et al., 1992), and the other new sequences of the present invention.

The above mentioned sets 1, 2 and 3 (see example 5) of primers were used, but only with set 1, PCR fragments could be obtained from all isolates (except for BE98, GB724, and CAR1/501). This set of primers amplified the sequence from nucleotide 379 to 957 encoding amino acids 127 to 319: 65 amino acids from the carboxyterminus of core and 128 amino acids of E1. With set 3, the core/E1 region from isolate NE92 and BE98 could be amplified, and with set 2, the core region of GB358, GB724, GB809, and CAM600 could be amplified. The amplification products were cloned as described in example 1. The following clones were obtained from the PCR fragments:

From isolate GB724, the clone with SEQ ID NO 193 from the core region.

From isolate NE92, the clone with SEQ ID NO 143

From isolate BE98, the clone from the core/E1 region of which part of the sequence has been analyzed and is given in SEQ ID NO 147,

From isolate CAM600, the clone with SEQ ID NO 167 from the E1 region, or SEQ ID NO 165 from the Core/E1 region as shown in Figure 3,

From isolate CAMG22, the clone with SEQ ID NO 171 from the E1 region as shown in Figure 4,

from isolate GB358, the clone with SEQ ID NO 191 in the core region,.

from isolate CAMG27, the clone with SEQ ID NO 173 from the core/E1 region,

from isolate GB438, the clone with SEQ ID NO 177 from the core/ E1 region,

from isolate CAR4/1205, the clone with SEQ ID NO 179 from the core/E1 region,

from isolate CAR1/901, the clone with SEQ ID NO 181 from the core/ E1 region,

from isolate GB809, the clone GB809-4 with SEQ ID NO 189 from the core/E1 region,

clone GB809-2 with SEQ ID NO 169 from the core/E1 region and the clone with SEQ ID NO 163 from the core region,

and from isolate BE100, the clone with SEQ ID NO 155 from the Core/E1 region as shown in Figure 4.

An alignment of these Core/E1 sequences with known Core/E1 sequences is presented in Figure 4. The deduced amino acid sequences with SEQ ID NO 144, 148, 164, 168, 170, 172, 174, 178, 180, 182, 190, 192, 194, 156, 166 are aligned with other prototype sequences in Figure 5. Again, type-specific variation mainly resides in the variable V regions, designated in the present invention, and therefore, type 2d, 3c and type 4-specific amino acids or V regions will be instrumental in diagnosis and therapeutics for HCV type (subtype) 2d, 3c or the different type 4 subtypes.

The NS5b region of isolates NE92, BE98, CAM600, CAMG22, GB438, CAR4/1205, CAR1/501, and BE96 was amplified with primers HCP206 and HCP207 (Table 7). The corresponding clones were cloned and sequenced as in example 1 and the corresponding sequences (of which BE98 was partly sequenced) received the following identification numbers:

NE92: SEQ ID NO 145

BE98: SEQ ID NO 149

CAM600: SEQ ID NO 201

CAMG22: SEQ ID NO 203

GB438: SEQ ID NO 207

CAR4/1205: SEQ ID NO 209

CAR1/501: SEQ ID NO 211

BE95: SEQ ID NO 159

BE96: SEQ ID NO 161

An alignment of these NS5b sequences with known NS5b sequences is presented in Figure 1. The deduced amino acid sequences with SEQ ID NO 146, 150, 202, 204, 206, 208, 210, 212, 160, 162 are aligned with other prototype sequences in Figure 2. Again, subtype-specific variations can be observed, and therefore, type 2d, 3c and type 4-specific amino acids or V regions will be instrumental in diagnosis and therapeutics for HCV type (subtype) 2d, 3c or the different type 4 subtypes.

Example 11 : Genotype-specific reactivity of anti-E1 antibodies (Serotyping)

E1 proteins were expressed from vaccinia virus constructs containing a core/E1 region extending from nucleotide positions 355 to 978 (Core/E1 clones described in previous examples including the primers HCP252 and HCP254), and expressed proteins from L119 (after the initiator methionine) to W326 of the HCV polyprotein. The expressed protein was modified upon expression in the appropriate host cells (e.g. HeLa, RK13, HuTK-, HepG2) by cleavage between amino acids 191 and 192 of the HCV polyprotein and by the addition of high-mannose type carbohydrate motifs. Therefore, a 30 to 32 kDa glycoprotein could be observed on western blot by means of detection with serum from patients with hepatitis C.

As a reference, a genotype 1b clone obtained from the isolate HCV-B was also expressed in an identical way as described above, and was expressed from recombinant vaccinia virus vvHCV-11A.

A panel of 104 genotyped sera was first tested for reactivity with a cell lysate containing type 1b protein expressed from the recombinant vaccinia virus vvHCV-11A, and compared with cell lysate of RK13 cells infected with a wild type vaccinia virus ('E1/WT'). The lysates were coated as a 1/20 dilution on a normal ELISA microtiter plate (Nunc maxisorb) and left to react with a 1/20 dilution of the respective sera. The panel consisted of 14 type 1a, 38 type 1b, 21 type 2, 21 type 3a, and 9 type 4 sera. Human antibodies were subsequently detected by a goat anti-human IgG conjugated with peroxidase and the enzyme activity was detected. The optical density values of the E1 and wild type lysates were divided and a factor 2 was taken as the cut-off. The results are given in the table A. Eleven out of 14 type 1a sera (79%), 25 out of 38 type 1b sera (66%), 6 out of 21 (29%), 5 out of 21 (24%), and none of the 9 type 4 or the type 5 serum reacted (0%). These experiments clearly show the high prevalence of anti-E1 antibodies reactive with the type 1 E1 protein in patients infected with type 1 (36/52 (69%)) (either type 1a or type 1b), but the low prevalence or absence in non-type 1 sera (11/52 (21%)).

TABLE A

serum	E1/WT
type 1a	
3748	3.15
3807	3.51
5282	1.99
9321	3.12
9324	2.76
9325	6.12
9326	10.56
9356	1.79
9388	3.5
8366	10.72
8380	2.27
10925	4.02
10936	5.04
10938	1.36

type 1b	
5205	2.25
5222	1.33
5246	1.24
5250	13.58
5493	0.87
5573	1.75
8243	1.77
8244	2.05
8316	1.21
8358	5.04
9337	14.47
9410	5
9413	5.51
10905	1.26
10919	5.00
10928	8.72
10929	8.26
10931	2.3
10932	4.41
44	2.37
45	3.14
46	4.37
47	5.68
48	2.97
49	1.18
50	9.85
51	4.51
52	1.11
53	5.20
54	0.98
55	1.48
56	1.06
57	3.85
58	7.6
59	3.28
60	3.23
61	7.82
62	1.92

type 2	
23	0.91
24	1.16
25	2.51
26	0.96
27	1.20
28	0.96
29	2.58
30	8.05
31	0.92
32	0.82
33	5.75
34	0.79
35	0.86
36	0.85
37	0.76
38	0.92
39	1.08
40	2.33
41	2.83
42	1.21
43	0.91
type 3	
1	6.88
2	1.47
3	3.06
4	6.52
5	10.24
6	2.72
7	1.11
8	1.54
9	1.60
10	1.21
11	1.07
12	1.00
13	0.85
14	0.96
15	0.51
16	1.00
17	1.09
18	0.99
19	1.04
20	1.04
21	0.96

type 4	
22	0.87
GB48	0.49
GB113	0.68
GB116	0.73
GB215	0.52
GB358	0.56
GB359	0.71
GB438	1.08
GB516	1.04
type 5	
BE95	0.86

Core/E1 clones of isolates BR36 (type 3a) and BE95 (type 5a) were subsequently recombined into the viruses vvHCV-62 and vvHCV-63, respectively. A genotyped panel of sera was subsequently tested onto cell lysates obtained from RK13 cells infected with the recombinant viruses vvHCV-62 and vvHCV-63. Tests were carried out as described above and the results are given in the table given below (TABLE B). From these results, it can clearly be seen that, although some cross-reactivity occurs (especially between type 1 and 3), the obtained values of a given serum are usually higher on its homologous E1 protein than on an E1 protein of another genotype. For type 5 sera, none of the 5 sera were reactive on type 1 or 3 E1 proteins, while 3 out of 5 were shown to contain anti-E1 antibodies when tested on their homologous type 5 protein. Therefore, in this simple test system, a considerable number of sera can already be serotyped. Combined with the reactivity to type-specific NS4 epitopes or epitopes derived from other type-specific parts of the HCV polyprotein, a serotyping assay may be developed for discriminating the major types of HCV. To overcome the problem of cross-reactivity, the position of cross-reactive epitopes may be determined by someone skilled in the art (e.g. by means of competition of the reactivity with synthetic peptides), and the epitopes evoking cross-reactivity may be left out of the composition to be included in the serotyping assay or may be included in sample diluent to outcompete cross-reactive antibodies.

TABLE B

serum	E1 ^{1b} /WT	E1 ^{3a} /WT	E1 ^{5a} /WT
type 1b			
8316	0.89	0.59	0.80
8358	2.22	2.65	1.96
9337	1.59	0.96	0.93
9410	16.32	9.60	3.62
9413	9.89	2.91	2.85
10905	1.04	0.96	1.05
10919	3.17	2.56	2.96
10928	4.39	2.28	2.07
10929	2.95	2.07	2.08
10931	3.11	1.49	2.11
5	0.86	0.86	0.96
6	3.48	1.32	1.32
7	6.76	4.00	3.77
8	10.88	3.44	4.04
9	1.76	1.88	1.58
10	9.88	7.48	7.20
11	8.48	8.99	8.45
12	0.76	0.72	0.76
13	5.04	5.67	5.37
14	10.48	10.54	11.22
15	5.18	1.62	1.65
type 3			
8332	3.39	4.22	0.66
10907	3.24	4.39	0.96
10908	0.99	0.94	0.98
10934	0.86	0.90	0.90
10927	2.58	2.71	2.44
8210	0.82	0.80	0.86
8344	1.09	6.66	1.17
8351	1.21	1.29	1.22
30	0.85	4.11	0.98
32	0.85	2.16	1.04
type 5			
BE110	0.78	0.95	1.54
BE95_	0.79	1.01	4.95
BE111	0.47	0.52	0.65
BE112	0.71	0.75	8.33
BE112	1.01	1.27	2.37
BE113	1.11	1.35	1.60

Table 5. Homologies of new HCV sequences with other known HCV types

Region (nucleotides)	Isolate (type)	1a HCV-1	1b HCV-J	2a HC-J6	2b HC-J8	3a T1 T7	3b T9 T10
Core (1-573)	PC (5)	83.8 (91.6)	84.8 (92.1)	82.6 (90.1)	82.4 (89.0)		
E1 (574-957)	HD10 (3) BR36 (3) BR33 (3) PC (5) GB358 (4a) GB549 (4b) GB809 (4c)	61.5 (68.0) 62.0 (66.4) 60.7 (67.2) 61.4 (64.0) 62.5 (69.1) 66.0 (72.2) 63.3 (69.1)	64.6 (68.8) 62.5 (67.2) 63.3 (68.0) 62.4 (64.8) 62.8 (65.9) 62.8 (69.8) 60.7 (64.3)	57.8 (55.5) 56.5 (53.9) 56.5 (54.7) 54.1 (49.6) 59.4 (54.0) 59.1 (56.4) 56.7 (53.2)	56.3 (59.4) 55.2 (58.6) 56.0 (58.6) 53.3 (47.2) 54.4 (54.0) 56.5 (54.0) 53.0 (51.6)		
NS3 (3856-4209)	PC (5)	74.7 (89)	76.1 (86.4)	76.1 (89.8)	78.0 (89.0)		
NS4 (4892-5292)	BR36 (3) HD 10 (3)	67.8 (78.5) 69.8 (74.6)	69.8 (75.1) 66.6 (69.7)	62.0 (67.5) 57.8 (59.9)	61.7 (66.0) 59.1 (59.9)		
NS4 (4936-5292)	PC (5)	61.3 (62.2)	63.0 (65.5)	52.9 (46.2)	54.3 (43.7)		
NS5b (8023-8235)	BR34 (3) BR36 (3) BR33 (3) GB358 (4a) GB549 (4b) GB809 (4c)	65.7 64.3 65.7 67.7 (76.1) 68.8 (76.1) 68.5 (73.5)	66.7 67.6 67.1 65.6 (77.0) 67.1 (77.0) 65.0 (73.5)	63.9 64.8 64.3 66.5 (70.8) 65.9 (71.7) 67.7 (69.9)	64.3 66.7 64.8 65.6 (71.7) 65.9 (74.4) 67.7 (73.5)	94.8 93.9 94.8 93.4 94.8 93.9	75.6 77.0 75.1 76.5 76.0 77.5

Shown are the nucleotide homologies (the amino-acid homology is given between brackets) for the region indicated in the left column.

Table 7

SEQ ID NO	Primer NO (polarity)	Sequence from 5' to 3'
63	HCPrl61(+)	5'-ACCGGAGGCCAGGAGAGTGATCTCCTCC-3'
64	HCPrl62(-)	5'-GGGCTGCTCTATCTCATCGACGCCATC-3'
65	HCPrl63(+)	5'-GCCAGAGGCTCGGAAGGCGATCAGCGCT-3'
66	HCPrl64(-)	5'-GAGTGCTCTGTCTCTCTCGACGCCGA-3'
67	HCPrl23(+)	5'-CTCATGGGGTACATTCGCT-3'
68	HCPrl54(-)	5'-CTATTACCAGTTTCATCATATCCCA-3'
69	HCPrl116(+)	5'-tttAAATACATCATGRCITGYATG-3'
70	HCPrl66(-)	5'-ctattaTTGTATCCCRCTGATGAARTTCCACAT-3'
71	HCPrl118(-)	5'-actagtcgactaYTGATICCRCTIATRWARTTCCACAT-3'
72	HCPrl117(+)	5'-tttAAATACATCGCIRCITGCATGCA-3'
73	HCPrl119(-)	5'-actagtcgactaRTTIGCLATIAGCCKRITTCATCCAYTG-3'
74	HCPrl131(+)	5'-ggaattctagaCCITCITGGGAYGARAYITGGAARTG-3'
75	HCPrl130(+)	5'-ggaattctagACIGCITAYCARGCIACIGTITGYGC-3'
76	HCPrl134(+)	5'-CATATAGATGCCCACTTCTCATC-3'
77	HCPrl3(+)	5'-GTGTGCCAGGACCATC-3'
78	HCPrl4(-)	5'-GACATGCATGTCATGATGA-3'
79	HCPrl152(+)	5'-TACGCCTCTTCTATATCGGTTGGGGCTG-3'
80	HCPrl52(+)	5'-atgTTGGGTAAGGTCATGATACCCT-3'
81	HCPrl41(+)	5'-CCCGGGAGGCTCTAGACCGTGCA-3'
82	HCPrl40(-)	5'-ctattaAAGATAGAGAAAGAGCAACCGGG-3'
124	HCPR206	5'-tggggatcccgatgatacccgctgcttga-3'
125	HCPR207	5'-ggcgaattcctggtcatagcctccgtgaa-3'
141	HCPR109	5'-tgggatatgatgatgaactggtc-3'
142	HCPR14	5'-ccaggtacaaccgaaccaattgcc-3'

Table 8 : NS4 SEROTYPING

serum	Type 1 NS4			Type 2 NS4			Type 3 NS4		
	1	5	7	1	5	7	1	5	7
type 1a									
101	3	3	3	-	1	3	+/-	+/-	3
102	1	+/-	2	-	-	2	-	-	1
103	1	3	3	-	+/-	3	-	+/-	3
104	3	3	3	2	2	3	3	+/-	2
105	3	3	3	-	2	2	+/-	+/-	2
106	3	1	1	-	1	2	+/-	+/-	+/-
107	3	3	3	-	2	2	2	-	1
108	3	3	3	-	+/-	2	+/-	1	2
109	3	3	3	+/-	2	3	1	-	3
110	3	3	3	-	+/-	1	-	-	3

serum	Type 1 NS4			Type 2 NS4			Type 3 NS4		
	1	5	7	1	5	7	1	5	7
type 1b									
111	+/-	+/-	-	-	-	-	-	-	-
112	-	2	3	-	-	2	-	-	3
113	2	3	3	-	-	1	-	-	3
114	2	3	3	1	+	2	+	1	3
115	3	3	3	-	+	3	-	-	3
116	3	3	3	-	+/-	1	-	-	1
117	3	3	-	-	+/-	1	-	-	1
118	1	2	3	3	+/-	+/-	+/-	-	3
119	+/-	2	2	+/-	+/-	2	+	1	2
120	-	3	3	-	+/-	+/-	-	-	-
121	3	3	3	3	2	2	2	2	3
122	3	3	1	+/-	1	2	2	1	1
123	3	3	2	-	1	2	2	1	1
124	3	3	3	-	+/-	2	-	-	2

serum	Type 1 NS4			Type 2 NS4			Type 3 NS4		
	1	5	7	1	5	7	1	5	7
125	3	3	3	1	1	3	2	1	3
126	1	2	2	1	1	1	1	1	1
127	3	2	2	-	+/-	1	+/-	+/-	+/-
128	3	3	3	-	+/-	1	2	+/-	+/-
129	2	3	3	-	-	3	-	-	3
130	-	2	1	+/-	-	-	-	-	-
131	-	1	1	+/-	-	-	-	-	+/-
132	-	-	-	+/-	-	+/-	+/-	-	-
133	3	3	3	-	1	3	-	1	3
134	-	2	2	-	-	-	-	-	-
135	3	3	3	1	+	2	2	1	3
136	-	3	3	+/-	+/-	+/-	+/-	-	3
137	+/-	+/-	+/-	+/-	+/-	+/-	+/-	-	-
138	3	3	3	+/-	2	2	1	+	3
type 2a									
139	3	-	-	3	3	+/-	1	-	-
140	+/-	-	-	3	3	3	3	-	-
141	2	-	-	2	1	+/-	2	-	-
142	-	-	-	-	+/-	-	-	-	-
143	-	+/-	+/-	1	2	1	1	+/-	+/-
144	1	1	+	1	3	2	1	1	2
145	-	+/-	+	3	1	2	2	+/-	+/-
146	-	-	-	+/-	+/-	-	-	-	-
147	-	+/-	-	3	1	3	-	-	-
148	-	-	-	+/-	-	-	+/-	-	-

serum	Type 1 NS4			Type 2 NS4			Type 3 NS4		
	1	5	7	1	5	7	1	5	7
type 2b									
149	-	+/-	+/-	3	3	3	2	+/-	+/-
type 3									
150	+/-	+/-	+/-	+/-	+/-	+/-	1	3	3
151	-	-	-	-	-	-	2	-	2
152	+/-	-	-	-	-	-	3	-	-
153	-	-	-	-	-	-	-	1	-
154	+/-	1	3	-	+/-	2	2	1	3
155	-	2	3	-	2	2	1	1	3
156	-	-	-	-	-	-	-	-	-
157	-	-	-	+/-	+/-	-	+/-	2	2
158	2	-	-	-	1	2	3	2	2
159	-	-	-	-	+/-	+/-	-	3	3
160	-	-	-	-	+/-	-	-	2	3
161	-	-	-	-	1	1	+/-	3	2
type 4									
162	1	-	-	1	-	-	-	-	-
163	2	-	-	2	+/-	+/-	+/-	-	-

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CLAIMS

1. A composition comprising or consisting of at least one polynucleic acid containing 8 or more contiguous nucleotides selected from at least one of the following HCV sequences:

- an HCV type 3 genomic sequence, more particularly in any of the following regions:
 - the region spanning positions 417 to 957 of the Core/E1 region of HCV subtype 3a,
 - the region spanning positions 4664 to 4730 of the NS3 region of HCV type 3,
 - the region spanning positions 4892 to 5292 of the NS3/4 region of HCV type 3,
 - the region spanning positions 8023 to 8235 of the NS5 region of HCV subtype 3a,
 - an HCV subtype 3c genomic sequence,
- an HCV subtype 2d genomic sequence,
- an HCV type 4 genomic sequence,
- the coding region of HCV subtype 5a,

with said nucleotide numbering being with respect to the numbering of HCV nucleic acids as shown in Table 1, and with said polynucleic acids containing at least one nucleotide difference with known HCV polynucleic acid sequences in the above-indicated regions, or the complement thereof.

2. A composition according to claim 1, wherein said polynucleic acids correspond to a nucleotide sequence selected from any of the following HCV genomic sequences:

- an HCV genomic sequence as having a homology of at least 67%, preferably more than 69%, most preferably 71% or more to any of the sequences as represented in SEQ ID NO 13, 15, 17, 19, 21, 23, 25 or 27 in the region spanning positions 417 to 957 of the Core/E1 region;
- an HCV genomic sequence as having a homology of at least 65%, preferably more than 67%, most preferably 69% or more to any of the sequences as represented in SEQ ID NO 19, 21, 23, 25 or 27 in the region spanning positions 574 to 957 of the E1 region;
- an HCV genomic sequence, having a homology of at least 79%, more preferably at least 81%, most preferably more than 83% or more to any of the sequences as represented in

- SEQ ID NO 147 in the region spanning positions 1 to 378 of the Core region ;
- an HCV genomic sequence having a homology of at least 74%, more preferably at least 76%, most preferably more than 78% or more to any of the sequences as represented in SEQ ID NO 13, 15, 17, 19, 21, 23, 25 or 27 in the region spanning positions 417 to 957 in the Core/E1 region;
 - an HCV genomic sequence having a homology of at least 74%, preferably more than 76%, most preferably 78% or more to any of the sequences as represented in SEQ ID NO 13, 15, 17, 19, 21, 23, 25 or 27 in the region spanning positions 574 to 957 in the E1 region;
 - an HCV genomic sequence having a homology of more than 73.5%, preferably more than 74%, most preferably 75% homology to any of the sequence as represented in SEQ ID NO 29 in the region spanning positions 4664 to 4730 of the NS3 region;
 - an HCV genomic sequence having a homology of more than 70%, preferably more than 72%, most preferably more than 74% homology to any of the sequences as represented in SEQ ID NO 29, 31, 33, 35, 37 or 39 in the region spanning positions 4892 to 5292 in the NS3/NS4 region;
 - an HCV genomic sequence having a homology of more than 95%, preferably 95.5%, most preferably 96% homology to any of the sequences as represented in SEQ ID NO 5, 7, 1, 3, 9 or 11 in the region spanning positions 8023 to 8235 of the NS5 region;
 - an HCV genomic sequence of the BR36 subgroup of HCV type 3a having a homology of more than 96%, preferably 96.5%, most preferably 97% homology to any of the sequences as represented in SEQ ID NO 5, 7, 1, 3, 9 or 11 in the region spanning positions 8023 to 8192 of the NS5B region;
 - an HCV genomic sequence having a homology of more than 79%, more preferably more than 81%, and most preferably more than 83% to the sequence as represented in SEQ ID NO 149 in the region spanning positions 7932 to 8271 in the NS5B region.
3. A composition according to claim 1, wherein said polynucleic acids correspond to a nucleotide sequence selected from any of the following HCV genomic sequences:
- an HCV genomic sequence having a homology of more than 85%, preferably more than 86%, most preferably more than 87% homology to any of the sequences as represented in SEQ ID NO 41, 43; 45, 47, 49, 51, 53 or 151 in the region spanning positions 1 to 573 of the Core region;

- an HCV genomic sequence having a homology of more than 61%, preferably more than 63%, most preferably more than 65% homology to any of the sequences as represented in SEQ ID NO 41, 43, 45, 47, 49, 51, 53, 153 or 155 in the region spanning positions 574 to 957 of the E1 region;
 - an HCV genomic sequence having a homology of more than 76.5%, preferably of more than 77%, most preferably of more than 78% homology with any of the sequences as represented in SEQ ID NO 55, 57, 197 or 199 in the region spanning positions 3856 to 4209 of the NS3 region;
 - an HCV genomic sequence having a homology of more than 68%, preferably of more than 70%, most preferably of more than 72% homology with the sequence as represented in SEQ ID NO 157 in the region spanning positions 980 to 1179 of the E1/E2 region;
 - an HCV genomic sequence having a homology of more than 57%, preferably more than 59%, most preferably more than 61% homology to any of the sequences as represented in SEQ ID NO 59 or 61 in the region spanning positions 4936 to 5296 of the NS4 region;
 - an HCV genomic sequence having a homology of more than 93%, preferably more than 93.5%, most preferably more than 94% homology to any of the sequences as represented in SEQ ID NO 159 or 161 in the region spanning positions 7932 to 8271 of the NS5B region.
4. A composition according to claim 1, wherein said polynucleic acids correspond to a nucleotide sequence selected from any of the following HCV genomic sequences:
- an HCV genomic sequence having a homology of more than 66%, preferably more than 68%, most preferably more than 70% homology in the E1 region spanning positions 574 to 957 to any of the sequences as represented in SEQ ID NO 118, 120 or 122 in the region spanning positions 1 to 957 of the Core/E1 region;
 - an HCV genomic sequence having a homology of more than 71%, preferably more than 72%, most preferably more than 74% homology to any of the sequences as represented in SEQ ID NO 118, 120 or 122 in the region spanning positions 379 to 957;
 - an HCV genomic sequence having a homology of more than 85%, preferably more than 86%, most preferably more than 86.5% homology to any of the sequences as represented in SEQ ID NO 183, 185 or 187 in the region spanning positions 379 to 957 of the E1 region;
 - an HCV genomic sequence having a homology of more than 81%, preferably more than

- 83%, most preferably more than 85% homology to the sequence as represented in SEQ ID NO 189 in the region spanning positions 379 to 957 of the E1 region;
- an HCV genomic sequence having a homology of more than 85%, preferably more than 87%, most preferably more than 89% homology to any of the sequences as represented in SEQ ID NO 167 or 169 in the region spanning positions 379 to 957 of the E1 region;
 - an HCV genomic sequence having a homology of more than 79%, preferably more than 81%, most preferably more than 83% homology to any of the sequences as represented in SEQ ID NO 171 or 173 in the region spanning positions 379 to 957 of the E1 region;
 - an HCV genomic sequence having a homology of more than 84%, preferably more than 86%, most preferably more than 88% homology to the sequence as represented in SEQ ID NO 175 in the region spanning positions 379 to 957 of the E1 region;
 - an HCV genomic sequence having a homology of more than 83%, preferably more than 85%, most preferably more than 87% homology to the sequence as represented in SEQ ID NO 177 in the region spanning positions 379 to 957 of the E1 region ;
 - an HCV genomic sequence having a homology of more than 76%, preferably more than 78%, most preferably more than 80% homology to the sequence as represented in SEQ ID NO 179 in the region spanning positions 379 to 957 of the E1 region;
 - an HCV genomic sequence having a homology of more than 84%, preferably more than 86%, most preferably more than 88% homology to the sequence as represented in SEQ ID NO 181 in the region spanning positions 379 to 957 of the E1 region ;
 - an HCV genomic sequence having a homology of more than 73%, preferably more than 75%, most preferably more than 77% homology to any of the sequences as represented in SEQ ID NO 106, 108, 110, 112, 114, or 116 in the region spanning positions 7932 to 8271 of the NS5 region ;
 - an HCV genomic sequence having a homology of more than 88%, preferably more than 89%, most preferably more than 90% homology to any of the sequences as represented in SEQ ID NO 106, 108, 110, or 112 in the region spanning positions 7932 to 8271 of the NS5 region;
 - an HCV genomic sequence having a homology of more than 88%, preferably more than 89%, most preferably more than 90% homology to any of the sequences as represented in SEQ ID NO 116 or 201 in the region spanning positions 7932 to 8271 of the NS5 region;
 - an HCV genomic sequence having a homology of more than 87%, preferably more than

- 89%, most preferably more than 90% homology to the sequence as represented in SEQ ID NO 203 in the region spanning positions 7932 to 8271 of the NS5 region;
- an HCV genomic sequence having a homology of more than 85%, preferably more than 87%, most preferably more than 89% homology to the sequence as represented in SEQ ID NO 114 in the region spanning positions 7932 to 8271 of the NS5 region;
 - an HCV genomic sequence having a homology of more than 86%, preferably more than 87%, most preferably more than 88% homology to the sequence as represented in SEQ ID NO 207 in the region spanning positions 7932 to 8271 of the NS5 region;
 - an HCV genomic sequence having a homology of more than 84%, preferably more than 86%, most preferably more than 88% homology to the sequence as represented in SEQ ID NO 209 in the region spanning positions 7932 to 8271 of the NS5 region;
 - an HCV genomic sequence having a homology of more than 81%, preferably more than 83%, most preferably more than 85% homology to the sequence as represented in SEQ ID NO 211 in the region spanning positions 7932 to 8271 of the NS5 region.
5. A composition according to claim 1, wherein said polynucleic acids correspond to a nucleotide sequence selected from any of the following HCV genomic sequences:
- an HCV genomic sequence having a homology of more than 78%, preferably more than 80%, most preferably more than 82% homology to the sequence as represented in SEQ ID NO 143 in the region spanning positions 379 to 957 of the Core/E1 region;
 - an HCV genomic sequence having a homology of more than 74%, preferably more than 76%, most preferably more than 78% homology to the sequence as represented in SEQ ID NO 143 in the region spanning positions 574 to 957;
 - an HCV genomic sequence having a homology of more than 87%, preferably more than 89%, most preferably more than 91% homology to the sequence as represented in SEQ ID NO 145 in the region spanning positions 7932 to 8271 of the NS5B region.
6. A composition according to any of claims 1 to 5, wherein said polynucleic acid is liable to act as a primer for amplifying the nucleic acid of a certain isolate belonging to the genotype from which the primer is derived.
7. A composition according to any of claims 1 to 5, wherein said polynucleic acid is able to act as a hybridization probe for specific detection and/or classification into types of a

nucleic acid containing said nucleotide sequence, with said oligonucleotide being possibly labelled or attached to a solid substrate.

8. Use of a composition according to any of claims 1 to 7 for *in vitro* detecting the presence of one or more HCV genotypes, more particularly for detecting the presence of a nucleic acid of any of the HCV genotypes having a nucleotide sequence as defined in any of claims 1 to 5, present in a biological sample liable to contain them, comprising at least the following steps:

- (i) possibly extracting sample nucleic acid,
- (ii) possibly amplifying the nucleic acid with at least one of the primers according to claim 6 or any other HCV type 2, HCV type 3, HCV type 4, HCV type 5 or universal HCV primer,
- (iii) hybridizing the nucleic acids of the biological sample, possibly under denatured conditions, and with said nucleic acids being possibly labelled during or after amplification, at appropriate conditions with one or more probes according to claim 7, with said probes being preferably attached to a solid substrate,
- (iv) washing at appropriate conditions,
- (v) detecting the hybrids formed,
- (vi) inferring the presence of one or more HCV genotypes present from the observed hybridization pattern.

9. A composition consisting of or comprising at least one peptide or polypeptide containing in its sequence a contiguous sequence of at least 5 amino acids of an HCV polypeptide encoded by any of the polynucleic acids according to any of claims 1 to 5.

10. A composition according to claim 9, wherein said contiguous sequence contains in its sequence at least one of the following amino acid residues:

L7, Q43, M44, S60, R67, Q70, T71, A79, A87, N106, K115, A127, A190, S130, V134, G142, I144, E152, A157, V158, P165, S177 or Y177, I178, V180 or E180 or F182, R184, I186, H187, T189, A190, S191 or G191, Q192 or L192 or I192 or V192 or E192, N193 or H193 or P193, W194 or Y194, H195, A197 or I197 or V197 or T197, V202, I203 or L203, Q208, A210, V212, F214, T216, R217 or D217 or E217 or V217, H218 or N218, H219 or V219 or L219, L227 or I227, M231 or E231 or Q231, T232 or D232 or A232 or K232, Q235

or I235, A237 or T237, I242, I246, S247, S248, V249, S250 or Y250, I251 or V251 or M251 or F251, D252, T254 or V254, L255 or V255, E256 or A256, M258 or F258 or V258, A260 or Q260 or S260, A261, T264 or Y264, M265, I266 or A266, A267, G268 or T268, F271 or M271 or V271, I277, M280 or H280, I284 or A284 or L84, V274, V291, N292 or S292, R293 or I293 or Y293, Q294 or R294, L297 or I297 or Q297, A299 or K299 or Q299, N303 or T303, T308 or L308, T310 or F310 or A310 or D310 or V310, L313, G317 or Q317, L333, S351, A358, A359, A363, S364, A366, T369, L373, F376, Q386, I387, S392, I399, F402, I403, R405, D454, A461, A463, T464, K484, Q500, E501, S521, K522, H524, N528, S531, S532, V534, F536, F537, M539, I546, C1282, A1283, H1310, V1312, Q1321, P1368, V1372, V1373, K1405, Q1406, S1409, A1424, A1429, C1435, S1436, S1456, H1496, A1504, D1510, D1529, I1543, N1567, D1556, N1567, M1572, Q1579, L1581, S1583, F1585, V1595, E1606 or T1606, M1611, V1612 or L1612, P1630, C1636, P1651, T1656 or I1656, L1663, V1667, V1677, A1681, H1685, E1687, G1689, V1695, A1700, Q1704, Y1705, A1713, A1714 or S1714, M1718, D1719, A1721 or T1721, R1722, A1723 or V1723, H1726 or G1726, E1730, V1732, F1735, I1736, S1737, R1738, T1739, G1740, Q1741, K1742, Q1743, A1744, T1745, L1746, E1747 or K1747, I1749, A1750, T1751 or A1751, V1753, N1755, K1756, A1757, P1758, A1759, H1762, T1763, Y1764, P2645, A2647, K2650, K2653 or L2653, S2664, N2673, F2680, K2681, L2686, H2692, Q2695 or L2695 or I2695, V2712, F2715, V2719 or Q2719, T2722, T2724, S2725, R2726, G2729, Y2735, H2739, I2748, G2746 or I2746, I2748, P2752 or K2752, P2754 or T2754, T2757 or P2757,

with said notation being composed of a letter representing the amino acid residue by its one-letter code, and a number representing the amino acid numbering according to Kato et al., 1990 as shown in Table 1.

11. A composition according to any of claims 9 or 10, wherein said contiguous sequence is selected from any of the following HCV amino acid sequences:

- a sequence having a homology of more than 72%, preferably more than 74%, and most preferably more than 77% homology to any of the amino acid sequences as represented in SEQ ID NO 14, 16, 18, 20, 22, 24, 26 or 28 in the region spanning positions 140 to 319 in the Core/E1 region;
- a sequence having a homology of more than 70%, preferably more than 72%, and most preferably more than 75% homology to any of the amino acid sequences as represented in SEQ ID NO 14, 16, 18, 20, 22, 24, 26 or 28 in the E1 region spanning positions 192 to

319;

- a sequence having a homology of more than 86%, preferably more than 88%, and most preferably more than 90% homology to the amino acid sequences as represented in SEQ ID NO 148 in the region spanning positions 1 to 110 in the Core region;
- a sequence having a homology of more than 76%, preferably more than 78%, most preferably more than 80% to any of the amino acid sequences as represented in SEQ ID NO 30, 32, 34, 36, 38 or 40 in the region spanning positions 1646 to 1764 in the NS3/NS4 region;
- a sequence having a homology of more than 81.5%, preferably more than 83%, and most preferably more than 86% homology to any of the amino acid sequences as represented in SEQ ID NO 14, 16, 18, 20, 22, 24, 26 or 28 in the E1 region spanning positions 192 to 319;
- a sequence having a homology of more than 86%, preferably more than 88%, most preferably more than 90% to the amino acid sequence as represented in SEQ ID NO 150 in the region spanning positions 2645 to 2757 in the NS5B region;

12. A composition according to any of claims 9 or 10, wherein said contiguous sequence is selected from any of the following HCV amino acid sequences:

- a sequence having a homology of more than 80%, preferably more than 82%, most preferably more than 84% homology to any of the amino acid sequences as represented in SEQ ID NO 118, 120, and 122 in the region spanning positions 127 to 319,
- a sequence having a homology of more than 73%, preferably more than 75%, most preferably more than 78% homology in the E1 region spanning positions 192 to 319 to any of the amino acid sequences as represented in SEQ ID NO 118, 120, and 122, in the region spanning positions 127 to 319,
- a sequence having more than 85%, preferably more than 86%, most preferably more than 87% homology to any of the amino acid sequences as represented in SEQ ID NO 118, 120 or 122, in the region spanning positions 192 to 319.

13. A composition according to any of claims 9 or 10, wherein said contiguous sequence is selected from any of the following HCV amino acid sequences:

- a sequence having more than 93%, preferably more than 94%, most preferably more than 95% homology in the region spanning Core positions 1 to 191 to any of the amino acid

sequences as represented in SEQ ID NO 42, 44, 46, 48, 50, 52, 54, or 152;

- a sequence having more than 73%, preferably more than 74%, most preferably more than 76% homology in the region spanning E1 positions 192 to 319 to any of the amino acid sequences as represented in SEQ ID NO 42, 44, 46, 48, 50, 52, 54, 154 or 156;
- a sequence spanning positions 1286 to 1403 of the NS3 region, with said sequence being characterized as having more than 90%, preferably more than 91%, most preferably more than 92% homology to any of the amino acid sequences represented in SEQ ID NO 56 to 58;
- a sequence spanning positions 1646 to 1764 of the NS3/4 region, with said sequence being characterized as having more than 66%, more particularly 68%, most particularly 70% or more homology to any of the amino acid sequences as represented in SEQ ID NO 60 or 62.

14. A composition according to any of claims 9 to 10, wherein said contiguous sequence is selected from any of the following HCV amino acid sequences:

- a sequence having a more than 83%, preferably more than 85%, most preferably more than 87% homology in the region spanning Core positions 1 to 319 to the amino acid sequence as represented in SEQ ID NO 144;
- a sequence having a more than 79%, preferably more than 81%, most preferably more than 84% homology in the region spanning E1 positions 192 to 319 to the amino acid sequence as represented in SEQ ID NO 144;
- a sequence having more than 95%, more particularly 96%, most particularly 97% or more homology to the amino acid sequence as represented in SEQ ID NO 146, in the region spanning positions 2645 to 2757 of the NS5B region.

15. A composition according to any of claims 9 to 14, wherein said sequence is selected from the following peptides:

QPTGRSWGQ (SEQ ID NO 93)
RSEGRTSWAQ (SEQ ID NO 220)
RTEGRTSWAQ (SEQ ID NO 221)
SRRQPIPRARTEGRSWAQ (SEQ ID NO 268)
LEWRNTSGLYVL (SEQ ID NO 83)
VNRYNASGIYHI (SEQ ID NO 126)

QHYRNISGIYHV (SEQ ID NO 127)
EHYRNASGIYHI (SEQ ID NO 128)
IHYRNASGIYHI (SEQ ID NO 224)
VPYRNASGIYHV (SEQ ID NO 84)
VNYRNASGIYHI (SEQ ID NO 225)
VNYRNASGVYHI (SEQ ID NO 226)
VNYHNTSGIYHL (SEQ ID NO 227)
QHYRNASGIYHV (SEQ ID NO 228)
QHYRNVSGIYHV (SEQ ID NO 229)
IHYRNASDGYI (SEQ ID NO 230)
LQVKNTSSSYMV (SEQ ID NO 231)
VYEADDVILHT (SEQ ID NO 85)
VYETEHHLHL (SEQ ID NO 129)
VYEADHHIMHL (SEQ ID NO 130)
VYETDHHILHL (SEQ ID NO 131)
VYEADNLILHA (SEQ ID NO 86)
VWQLRAIVLHV (SEQ ID NO 232)
VYEADYHILHL (SEQ ID NO 233)
VYETDNHILHL (SEQ ID NO 234)
VYETENHILHL (SEQ ID NO 235)
VFETVHHILHL (SEQ ID NO 236)
VFETEHHLHL (SEQ ID NO 237)
VFETDHHIMHL (SEQ ID NO 238)
VYETENHILHL (SEQ ID NO 239)
VYEADALILHA (SEQ ID NO 240)
VQDGTSTCWTPV (SEQ ID NO 87)
VQDGTNSACWTPV (SEQ ID NO 241)
VRVGNQSRCWVAL (SEQ ID NO 132)
VRTGNTSRCWVPL (SEQ ID NO 133)
VRAGNVSRCWTPV (SEQ ID NO 134)
EEKGNISRCWIPV (SEQ ID NO 242)
VKTGNQSRCWVAL (SEQ ID NO 243)
VRTGNQSRCWVAL (SEQ ID NO 244)

VKTGNQSRCWIAL (SEQ ID NO 245)
VKTGNVSRWCWIP (SEQ ID NO 247)
VKTGNVSRCWISL (SEQ ID NO 248)
VRKDNVSRCWVQI (SEQ ID NO 249)
VRYVGATTAS (SEQ ID NO 89)
APYIGAPLES (SEQ ID NO 135)
APYVGAPLES (SEQ ID NO 136)
AVSMDAPLES (SEQ ID NO 137)
APSLGAVTAP (SEQ ID NO 90)
APSGAVTAP (SEQ ID NO 250)
VSQPGALTKG (SEQ ID NO 251)
VKYVGATTAS (SEQ ID NO 252)
APYIGAPVES (SEQ ID NO 253)
AQHLNAPLES (SEQ ID NO 254)
SPYVGAPLEP (SEQ ID NO 255)
SPYAGAPLEP (SEQ ID NO 256)
APYLGAPLEP (SEQ ID NO 257)
APYLGAPLES (SEQ ID NO 258)
APYVGAPLES (SEQ ID NO 259)
VPYLGAPLTS (SEQ ID NO 260)
APHLRAPLSS (SEQ ID NO 261)
APYLGAPLTS (SEQ ID NO 262)
RPRRHQTVQT (SEQ ID NO 91)
QPRRHWTQD (SEQ ID NO 138)
RPRRHWTQD (SEQ ID NO 139)
RPRQHATVQN (SEQ ID NO 92)
RPRQHATVQD (SEQ ID NO 263)
SPQHHKFVQD (SEQ ID NO 264)
RPRRLWTTQE (SEQ ID NO 265)
PPRIHETTQD (SEQ ID NO 266)
TISYANGSGPSDDK (SEQ ID NO 267)

16. Recombinant vector, particularly for cloning and/or expression, with said recombinant

vector comprising a vector sequence, an appropriate prokaryotic, eukaryotic or viral promoter sequence followed by the nucleotide sequences as defined in claims 1 to 5, with said recombinant vector allowing the expression of any one of the HCV type 2 and/or HCV type 3 and/or type 4 and/or type 5 derived polypeptides according to any of claims 9 to 15 in a prokaryotic, or eukaryotic host, or in living mammals when injected as naked DNA, and more particularly a recombinant vector allowing the expression of any of the following HCV type 2, HCV type 3, type 4 or type 5 polypeptides spanning the following amino acid positions:

- a polypeptide starting at position 1 and ending at any position in the region between positions 70 and 326, more particularly a polypeptide spanning positions 1 to 70, 1 to 85, positions 1 to 120, positions 1 to 150, positions 1 to 191, positions 1 to 200, for expression of the Core protein, and positions 1 to 263, positions 1 to 326, for expression of the Core and E1 protein;
- a polypeptide starting at any position in the region between positions 117 and 192, and ending at any position in the region between positions 263 and 326, more particularly from positions 119 to 326, for expression of E1, or forms that have the putative membrane anchor deleted (positions 264 to 293 plus or minus 8 amino acids);
- a polypeptide starting at any position in the region between positions 1556 and 1688, and ending at any position in the region between positions 1739 and 1764, for expression of the NS4 regions, more particularly a polypeptide starting at position 1658 and ending at position 1711 for expression of the NS4a antigen, and more particularly, a polypeptide starting at position 1712 and ending between positions 1743 and 1972, for example 1712-1743, 1712-1764, 1712-1782, 1712-1972, 1712 to 1782 and 1902 to 1972 for expression of the NS4b protein or parts thereof.

17. A composition according to any of claims 9 to 15, wherein said polypeptide is a recombinant polypeptide expressed by means of an expression vector as defined in claim 16.

18. A composition according to any of claims 9 to 15 or 16, for use in a method for immunizing a mammal, preferably humans, against HCV comprising administering a sufficient amount of the composition possibly accompanied by pharmaceutically acceptable adjuvants, to produce an immune response, more particularly a vaccine composition including HCV type 3 polypeptides derived from the E1, Core, or NS4 region and/or type 4 and/or type 5 and/or type 2 polypeptides.

19. Antibody raised upon immunization with a composition according to any of claims 9 to 15, 17 or 18, by means of a process according to claim 18, with said antibody being reactive with any of the polypeptides as defined in any of claims 9 to 15, 17 or 18.
20. Process for detecting *in vitro* HCV present in biological sample liable to contain it, comprising at least the following steps:
- (i) contacting the biological sample to be analyzed for the presence of HCV antibodies with any of the compositions according to claims 9 to 15, 17 or 18, preferentially in an immobilized form under appropriate conditions which allow the formation of an immune complex, wherein said polypeptide is preferentially in the form of a biotinylated polypeptide and is covalently bound to a solid substrate by means of streptavidin or avidin complexes,
 - (ii) removing unbound components,
 - (iii) incubating the immunocomplexes formed with heterologous antibodies, which specifically bind to the antibodies present in the sample to be analyzed, with said heterologous antibodies having conjugated to a detectable label under appropriate conditions,
 - (iv) detecting the presence of said immunocomplexes visually or by means of densitometry and inferring the HCV serotype(s) present from the observed hybridization pattern.
21. Use of a composition according to any of claims 9 to 15, 17 or 18, for incorporation into a serotyping assay for detecting one or more serological types of HCV present in a biological sample liable to contain it, more particularly for detecting E1 and NS4 antigens or antibodies of the different types to be detected combined in one assay format, comprising at least the following steps:
- (i) contacting the biological sample to be analyzed for the presence of HCV antibodies or antigens of one or more serological types, with at least one of the compositions according to claims 9 to 15, 17 or 18 in an immobilized form under appropriate conditions which allow the formation of an immunocomplex, (wherein said polypeptide is preferentially in the form of a biotinylated polypeptide and is covalently bound to a solid substrate by means of streptavidin or avidin complexes),

- (ii) removing unbound components,
- (iii) incubating the immunocomplexes formed with heterologous antibodies, which specifically bind to the antibodies present in the sample to be analyzed, with said heterologous antibodies having conjugated to a detectable label under appropriate conditions,
- (iv) detecting the presence of said immunocomplexes visually or by means of densitometry and inferring the HCV serological types present from the observed binding pattern.

22. A kit for determining the presence of HCV genotypes as defined in any of claims 1 to 5 present in a biological sample liable to contain them, comprising:

- possibly at least one primer composition containing any primer selected from those defined in claim 6 or any other HCV type 2 and/or HCV type 3 and/or HCV type 4 and/or HCV type 5, or universal HCV primers,
- at least one probe composition according to claim 7, preferably in combination with other polypeptides or peptides from HCV type 1, type 2 or other types of HCV, with said probes being preferentially immobilized on a solid substrate, and more preferentially on one and the same membrane strip,
- a buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the possibly amplified products to be carried out,
- a means for detecting the hybrids resulting from the preceding hybridization,
- possibly also including an automated scanning and interpretation device for inferring the HCV genotype(s) present in the sample from the observed hybridization pattern.

23. A kit for determining the presence of HCV antibodies according to any of claims 9 to 15, 17 or 18 present in a biological sample liable to contain them, comprising:

- at least one polypeptide composition according to any of claims 9 to 15, 17 or 18, with said polypeptides being preferentially immobilized on a solid substrate, and more preferentially on one and the same membrane strip,
- a buffer or components necessary for producing the buffer enabling binding reaction between these polypeptides and the antibodies against HCV present in the biological sample,
- a means for detecting the immune complexes formed in the preceding binding

reaction,

- possibly also including an automated scanning and interpretation device for inferring the HCV genotype present in the sample from the observed binding pattern.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Innogenetics sa.
- (B) STREET: Industriepark Zwijnaarde 7, box 4
- (C) CITY: Ghent
- (E) COUNTRY: Belgium
- (F) POSTAL CODE (ZIP): B-9052
- (G) TELEPHONE: 00 32 9 241 07 11
- (H) TELEFAX: 00 32 9 241 07 99

- (ii) TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy.

- (iii) NUMBER OF SEQUENCES: 270

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR34-4-20

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTC	ACG	GAA	CGG	CTT	TAC	TGC	GGG	GGC	CCT	ATG	TTC	AAC	AGC	AAG	GGG	48
Leu	Thr	Glu	Arg	Leu	Tyr	Cys	Gly	Gly	Pro	Met	Phe	Asn	Ser	Lys	Gly	
1				5					10					15		
GCC	CAG	TGT	GGT	TAT	CGC	CGC	TGC	CGT	GCC	AGT	GGA	GTT	CTG	CCT	ACC	96
Ala	Gln	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Pro	Thr	

96																
20				25				30								
AGC	TTC	GGC	AAC	ACA	ATC	ACT	TGC	TAC	ATC	AAG	GCC	ACA	GCG	GCT	GCA	144
Ser	Phe	Gly	Asn	Thr	Ile	Thr	Cys	Tyr	Ile	Lys	Ala	Thr	Ala	Ala	Ala	
35				40				45								
AGG	GCC	GCA	GGC	CTC	CGG	AAC	CCG	GAC	TTT	CTT	GTC	TGC	GGA	GAT	GAT	192
Arg	Ala	Ala	Gly	Leu	Arg	Asn	Pro	Asp	Phe	Leu	Val	Cys	Gly	Asp	Asp	
50				55				60								
CTG	GTC	GTG	GTG	GCT	GAG	AGT										213
Leu	Val	Val	Val	Ala	Glu	Ser										
65				70												

(2) INFORMATION FOR SEO ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
1 5 10 15
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
20 25 30
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
35 40 45
Arg Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp
50 55 60
Leu Val Val Val Ala Glu Ser
65 70

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR36-23-18

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTC	ACG	GAA	CGG	CTT	TAC	TGC	GGG	GGC	CCT	ATG	TTC	AAC	AGC	AAG	GGG	48
Leu	Thr	Glu	Arg	Leu	Tyr	Cys	Gly	Gly	Pro	Met	Phe	Asn	Ser	Lys	Gly	
1				5					10					15		
GCC	CAG	TGT	GGT	TAT	CGC	CGC	TGC	CGT	GCC	AGT	GGA	GTT	CTG	CCT	ACC	96
Ala	Gln	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Pro	Thr	
	20							25					30			
AGC	TTC	GGC	AAC	ACA	ATC	ACT	TGC	TAC	ATC	AAG	GCC	ACA	CGG	GCT	GCA	144
Ser	Phe	Gly	Asn	Thr	Ile	Thr	Cys	Tyr	Ile	Lys	Ala	Thr	Ala	Ala	Ala	
	35						40					45				
AGG	GCC	GCA	GGC	CTC	CGG	AAC	CCG	GAC	TTT	CTT	GTC	TGC	GGA	GAT	GAT	192
Arg	Ala	Ala	Gly	Leu	Arg	Asn	Pro	Asp	Phe	Leu	Val	Cys	Gly	Asp	Asp	
	50					55					60					
CTG	GTC	GTG	GTG	GCT	GAG	AGT										213
Leu	Val	Val	Val	Ala	Glu	Ser										
65					70											

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Leu	Thr	Glu	Arg	Leu	Tyr	Cys	Gly	Gly	Pro	Met	Phe	Asn	Ser	Lys	Gly	
1				5					10					15		
Ala	Gln	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Pro	Thr	
	20						25					30				
Ser	Phe	Gly	Asn	Thr	Ile	Thr	Cys	Tyr	Ile	Lys	Ala	Thr	Ala	Ala	Ala	
	35					40					45					
Arg	Ala	Ala	Gly	Leu	Arg	Asn	Pro	Asp	Phe	Leu	Val	Cys	Gly	Asp	Asp	
	50					55					60					
Leu	Val	Val	Val	Ala	Glu	Ser										
65					70											

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: BR36-23-18
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTC ACG GAG CGG CTT TAC TGC GGG GGC CCT ATG TTT AAC AGC AAG GGG	48
Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly	
1 5 10 15	
GCC CAG TGT GGT TAT CGC CGT TGC CGT GCC AGT GGA GTT CTG CCT ACC	96
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr	
20 25 30	
AGC TTC GGC AAC ACA ATC ACT TGT TAC ATC AAA GCC ACA GCG GCC GCA	144
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala	
35 40 45	
AAA GCC GCA GGC CTC CGG AGC CCG GAC TTT CTT GTC TGC GGA GAT GAT	192
Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp	
50 55 60	
CTG GTC GTG GTG GCT GAG AGT	213
Leu Val Val Val Ala Glu Ser	
65 70	

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
1 5 10 15
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
20 25 30
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
35 40 45

99

Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp
 50 55 60

Leu Val Val Val Ala Glu Ser
 65 70

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-23-20

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTC	ACG	GAG	CGG	CTT	TAC	TGC	GGG	GGC	CCT	ATG	TTT	AAC	AGC	AAA	GGG	48
Leu	Thr	Glu	Arg	Leu	Tyr	Cys	Gly	Gly	Pro	Met	Phe	Asn	Ser	Lys	Gly	
1				5				10				15				
GCC	CAG	TGT	GGT	TAT	CGC	CGT	TGC	CGT	GCC	AGT	GGA	GTT	CTG	CCT	ACC	96
Ala	Gln	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Pro	Thr	
			20				25					30				
AGC	TTC	GGC	AAC	ACA	ATC	ACT	TGT	TAC	ATC	AAA	GCC	ACA	GCG	GCC	GCA	144
Ser	Phe	Gly	Asn	Thr	Ile	Thr	Cys	Tyr	Ile	Lys	Ala	Thr	Ala	Ala	Ala	
			35				40					45				
AAA	GCC	GCA	GGC	CTC	CGG	AGC	CCG	GAC	TTT	CTT	GTC	TGC	GGA	GAT	GAT	192
Lys	Ala	Ala	Gly	Leu	Arg	Ser	Pro	Asp	Phe	Leu	Val	Cys	Gly	Asp	Asp	
			50				55					60				
CTG	GTC	GTG	GTG	GCT	GAG	AGT										213
Leu	Val	Val	Val	Ala	Glu	Ser										
65				70												

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
 1             5             10             15

Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
      20             25             30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
      35             40             45

Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp
      50             55             60

Leu Val Val Val Ala Glu Ser
65             70

```

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR33-2-17

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```

CTC ACG GAG CGG CTT TAC TGC GGG GGC CCT ATG TTC AAC AGC AAG GGG      48
Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
 1             5             10             15

GCC CAG TGT GGT TAT CGC CGT TGT CGT GCC AGT GGA GTT CTG CCT ACC      96
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
      20             25             30

AGT TTC GGC AAC ACA ATC ACT TGT TAC ATC AAG GCC ACA GCG GCT GCA      144
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
      35             40             45

AAA GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTT TGC GGA GAT GAT      192

```

101

Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp
 50 55 60

TTG GTC GTG GTG GCT GAG AGT
 Leu Val Val Val Ala Glu Ser
 65 70

213

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
 1 5 10 15

Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
 20 25 30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
 35 40 45

Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp
 50 55 60

Leu Val Val Val Ala Glu Ser
 65 70

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR33-2-21

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CTC	ACG	GAG	CGG	CTT	TAC	TGC	GGG	GGC	CCT	ATG	TTC	AAC	AGC	AAG	GGG	48
Leu	Thr	Glu	Arg	Leu	Tyr	Cys	Gly	Gly	Pro	Met	Phe	Asn	Ser	Lys	Gly	
1				5					10					15		
GCC	CAG	TGT	GGT	TAT	CGC	CGT	TGT	CGT	GCC	AGT	GGA	GTT	CTG	CCT	ACC	96
Ala	Gln	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Pro	Thr	
			20					25					30			
AGT	TTC	GGC	AAC	ACA	ATC	ACT	TGT	TAC	ATC	AAG	GCC	ACA	CGC	GCT	GCA	144
Ser	Phe	Gly	Asn	Thr	Ile	Thr	Cys	Tyr	Ile	Lys	Ala	Thr	Ala	Ala	Ala	
			35					40					45			
AAA	GCC	GCA	GGC	CTC	CGG	AAC	CCG	GAC	TTT	CTT	GTT	TGC	GGA	GAT	GAT	192
Lys	Ala	Ala	Gly	Leu	Arg	Asn	Pro	Asp	Phe	Leu	Val	Cys	Gly	Asp	Asp	
			50					55				60				
TTG	GTC	GTG	GTG	GCT	GAG	AGT										213
Leu	Val	Val	Val	Ala	Glu	Ser										
65						70										

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Leu	Thr	Glu	Arg	Leu	Tyr	Cys	Gly	Gly	Pro	Met	Phe	Asn	Ser	Lys	Gly
1				5					10					15	
Ala	Gln	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Pro	Thr
			20					25					30		
Ser	Phe	Gly	Asn	Thr	Ile	Thr	Cys	Tyr	Ile	Lys	Ala	Thr	Ala	Ala	Ala
			35					40					45		
Lys	Ala	Ala	Gly	Leu	Arg	Asn	Pro	Asp	Phe	Leu	Val	Cys	Gly	Asp	Asp
			50					55				60			
Leu	Val	Val	Val	Ala	Glu	Ser									
65						70									

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HD10-2-5

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

C GTC GGC GCT CCT GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly 1 5 10 15	46
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro 20 25 30	94
GGT TGC TCC TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile 35 40 45	142
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAC ACG TCT GGC CTC TAT GTC His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val 50 55 60	190
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT GAC Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp 65 70 75	238
GTT ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT CAG GAC GGT AAT Val Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn 80 85 90 95	286
ACA TCT GCG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AGG TAC Thr Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr 100 105 110	334
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGG CAT GTA GAC ATG TTG GTG Val Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Met Leu Val 115 120 125	382
GGC GCG GCC ACG ATG TGC TCT GCT CTC TAC GTG GGT GAT ATG TGT GGG Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly 130 135 140	430
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His 145 150 155	478
CAA ACG GTC CAG ACC TGT AAC TGC TCA CTG TAC CCA GGC CAT CTT TCA Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser 160 165 170 175	526

GGA CAC CGA ATG GCT
 Gly His Arg Met Ala
 180

541

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val
 1 5 10 15
 Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly
 20 25 30
 Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His
 35 40 45
 Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu
 50 55 60
 Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val
 65 70 75 80
 Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr
 85 90 95
 Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
 100 105 110
 Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Met Leu Val Gly
 115 120 125
 Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala
 130 135 140
 Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln
 145 150 155 160
 Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
 165 170 175
 His Arg Met Ala
 180

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
(B) CLONE: HD10-2-14
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

C GTC GGC GCT CCT GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATC TTC CTT CCT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Pro Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAC ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT CAG GAC GGT AAT	286
Val Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCT GCG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AGG TAC	334
Thr Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr	
100 105 110	
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGG CAT GTA GAC ATA TIG GTG	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val	
115 120 125	
GGC GCG GCC ACA ATG TGC TCT GCT CTC TAC GTG GGT GAT ATG TGT GGG	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130 135 140	
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT	478
Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His	
145 150 155	
CAA ACG GTC CAG ACC TGT AAC TGC TCA CTG TAC CCA GGC CAT CTT TCA	526

Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser
160 165 170 175

GGA CAC CGA ATG GCT
Gly His Arg Met Ala
180

541

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val
1 5 10 15
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly
20 25 30
Cys Ser Phe Ser Ile Phe Leu Pro Ala Leu Phe Ser Cys Leu Ile His
35 40 45
Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu
50 55 60
Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val
65 70 75 80
Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr
85 90 95
Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
100 105 110
Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val Gly
115 120 125
Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala
130 135 140
Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln
145 150 155 160
Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
165 170 175
His Arg Met Ala
180

(2) INFORMATION FOR SEQ ID NO: 17 :

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 541 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HD10-2-21

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

C GTC GGC GCT CCT GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAC ACG TCT GGC CTC TAC GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT CAG GAC GGT AAT	286
Val Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCT GCG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AGG TAC	334
Thr Ser Ala Cys Thr Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr	
100 105 110	
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGG CAT GTA GAC ATA TTG GTG	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val	
115 120 125	
GGC GCG GCC ACG ATG TGC TCT GCT CTC TAC GTG GGT GAT ATG TGT GGG	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130 135 140	

GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT 478
 Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His
 145 150 155
 CAA ACG GTC CAG ACC TGT AAC TGC TCA CTG TAC CCA GGC CAT CTT TCA 526
 Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser
 160 165 170 175
 GGA CAC CGA ATG GCT 541
 Gly His Arg Met Ala
 180

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val
 1 5 10 15
 Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly
 20 25 30
 Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His
 35 40 45
 Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu
 50 55 60
 Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val
 65 70 75 80
 Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr
 85 90 95
 Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
 100 105 110
 Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val Gly
 115 120 125
 Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala
 130 135 140
 Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln
 145 150 155 160
 Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
 165 170 175
 His Arg Met Ala

180

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 541 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE:

(B) CLONE: BR36-9-13

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATT TTC CTT CTT GCT CTG TTC TCT TGC TTA ATT	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAC GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGC ATA CCT TGT GTC CAG GAC GGC AAT	286
Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCC ACG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AAG TAC	334
Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr	
100 105 110	
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val	
115 120 125	

GGC GCG GCC ACG ATG TGC TCA GCG CTC TAC GTG GGT GAT ATG TGT GGG	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130 135 140	
GGC GTC TTC CTT GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT	478
Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His	
145 150 155	
CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA	526
Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser	
160 165 170 175	
GGA CAT CGA ATG GCT	541
Gly His Arg Met Ala	
180	

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val	
1 5 10 15	
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly	
20 25 30	
Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His	
35 40 45	
Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu	
50 55 60	
Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val	
65 70 75 80	
Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn Thr	
85 90 95	
Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr Val	
100 105 110	
Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly	
115 120 125	
Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala	
130 135 140	
Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln	
145 150 155 160	
Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly	

165

170

175

His Arg Met Ala
180

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 541 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-9-20

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATT TTC CTT CTT GCT CTG TTC TCT TGC TTA ATT	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAC GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGC ATA CCT TGT GTC CAG GAC GGC AAT	286
Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCC ACG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AAG TAC	334
Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr	
100 105 110	

GTC GGA GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val	
115 120 125	
GGC GCG GCC ACG ATG TGC TCT GCG CTC TAC GTG GGT GAC ATG TGT GGG	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130 135 140	
GCT GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT	478
Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His	
145 150 155	
CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA	526
Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser	
160 165 170 175	
GGA CAT CGA ATG GCT	541
Gly His Arg Met Ala	
180	

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val	
1 5 10 15	
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly	
20 25 30	
Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His	
35 40 45	
Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu	
50 55 60	
Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val	
65 70 75 80	
Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn Thr	
85 90 95	
Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr Val	
100 105 110	
Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly	
115 120 125	
Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala	
130 135 140	

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln
 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
 165 170 175

His Arg Met Ala
 180

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 541 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: BR33-1-10

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAG GAC GGG ATA AAC TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT GGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGT AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC GCG CCC GGC TGT GTA CCT TGT GTC CAG GAC GGC AAT	286
Val Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	

ACG TCT ACA TGC TGG ACC CCA GTA ACA CCT ACA GTG GCA GTC AGG TAC	334
Thr Ser Thr Cys Trp Thr Pro Val Thr Thr Val Ala Val Arg Tyr	
100 105 110	
GTG GGG GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTG TTA GTA	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val	
115 120 125	
GGC GCG GCC ACG ATG TGC TCT GCG CTT TAC GTG GGT GAT ATG TGT GGS	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130 135 140	
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCC CGC CGC CAT	478
Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His	
145 150 155	
CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA	526
Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser	
160 165 170 175	
GGA CAT CGC ATG GCT	541
Gly His Arg Met Ala	
180	

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val	
1 5 10 15	
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly	
20 25 30	
Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His	
35 40 45	
Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu	
50 55 60	
Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val	
65 70 75 80	
Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr	
85 90 95	
Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val	
100 105 110	
Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly	

115	120	125
Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala		
130	135	140
Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln		
145	150	155
160		
Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly		
165	170	175

His Arg Met Ala
180

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 541 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: BR33-1-19

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

C	GTC	GGC	GCT	CCC	GTA	GGA	GGC	GTC	GCA	AGA	GCC	CTT	GCG	CAT	GGC	46
Val	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly		
1					5				10					15		
GTG	AGG	GCC	CTT	GAG	GAC	GGG	ATA	AAC	TTC	GCA	ACA	GGG	AAT	TTG	CCC	94
Val	Arg	Ala	Leu	Glu	Asp	Gly	Ile	Asn	Phe	Ala	Thr	Gly	Asn	Leu	Pro	
			20					25					30			
GGT	TGC	TCT	TTT	TCT	ATC	TTC	CTT	CTT	GCT	CTG	TTC	TCT	TGC	TTA	ATC	142
Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Phe	Ser	Cys	Leu	Ile	
			35				40					45				
CAT	CCA	GCA	GCT	GGT	CTA	GAG	TGG	CGG	AAT	ACG	TCT	GGC	CTC	TAT	GTC	190
His	Pro	Ala	Ala	Gly	Leu	Glu	Trp	Arg	Asn	Thr	Ser	Gly	Leu	Tyr	Val	
		50					55				60					
CTT	ACC	AAC	GAC	TGT	TCC	AAT	AGT	AGT	ATT	GTG	TAT	GAG	GCC	GAT	GAC	238
Leu	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asp	
		65					70				75					

GTT ATT CTG CAC GCG CCC GGC TGT GTA CCT TGT GTC CAG GAC GGC AAT	286
Val Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACG TCT ACA TGC TGG ACC CCA GTA ACA CCT ACA GTG GCA GTC AGG TAC	334
Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr	
100 105 110	
GTC GGG GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTG TTA GTA	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val	
115 120 125	
GGC GCG GCC ACG ATG TGC TCT GCG CTT TAC GTG GGT GAT ATG TGT GGG	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130 135 140	
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCC CGC CGC CAT	478
Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His	
145 150 155	
CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA	526
Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser	
160 165 170 175	
GGA CAT CGA ATG GCT	541
Gly His Arg Met Ala	
180	

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val	
1 5 10 15	
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly	
20 25 30	
Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His	
35 40 45	
Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu	
50 55 60	
Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val	
65 70 75 80	
Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr	
85 90 95	

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
 100 105 110

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Val Gly
 115 120 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala
 130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln
 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
 165 170 175

His Arg Met Ala
 180

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 541 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: BR33-1-20
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..541
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAG GAC GGG ATA AAC TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCT TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT GGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	

CTT ACC AAC GAC TGT TCC AAT AGT AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC GCG CCC GGC TGT GTA CCT TGT GTC CAG GAC GGC AAT	286
Val Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACG TCT ACA TGC TGG ACC CCA GTA ACA CCT ACA GTG GCA GTC AGG TAC	334
Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr	
100 105 110	
GTC GGG GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTG TTA GTA	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val	
115 120 125	
GGC GCG GCC ACG ATG TGC TCT GCG CTT TAC GTG GGT GAT ATG TGT GGG	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130 135 140	
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCC GCG CGC CAT	478
Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His	
145 150 155	
CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA	526
Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser	
160 165 170 175	
GGA CAT CGA ATG GCT	541
Gly His Arg Met Ala	
180	

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val	
1 5 10 15	
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly	
20 25 30	
Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His	
35 40 45	
Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu	
50 55 60	
Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val	
65 70 75 80	

Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr
85 90 95

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
100 105 110

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly
115 120 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala
130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln
145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
165 170 175

His Arg Met Ala
180

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vii) IMMEDIATE SOURCE:
(B) CLONE: HCC1153

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 3..287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TA GAC TTT TGG GAG AGC GTC TTC ACT GGA CTA ACT CAC ATA GAT GCC	47
Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala	
1 5 10 15	
CAC TTT CTG TCA CAG ACT AAG CAG CAG GGA CTC AAC TTC TCG TTC CTG	95
His Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu	
20 25 30	
ACT GCC TAC CAA GCC ACT GTG TGC GCT CGC GCG CAG GCT CCT CCC CCA	143
Thr Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro	
35 40 45	
AGT TGG GAC GAG ATG TGG AAG TGT CTC GTA CGG CTT AAG CCA ACA CTA	191

Ser	Trp	Asp	Glu	Met	Trp	Lys	Cys	Leu	Val	Arg	Leu	Lys	Pro	Thr	Leu		
		50					55					60					
CAT	GGA	CCT	ACG	CCT	CTT	CTA	TAT	CGG	TTG	GGG	CCT	GTC	CAA	AAT	GAA		239
His	Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Pro	Val	Gln	Asn	Glu		
		65				70					75						
ATC	TGC	TTG	ACA	CAC	CCC	ATC	ACA	AAA	TAC	ATC	ATG	GCA	TGC	ATG	TCA		287
Ile	Cys	Leu	Thr	His	Pro	Ile	Thr	Lys	Tyr	Ile	Met	Ala	Cys	Met	Ser		
	80				85					90					95		

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Asp	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	Ile	Asp	Ala	His
1				5					10					15	
Phe	Leu	Ser	Gln	Thr	Lys	Gln	Gln	Gly	Leu	Asn	Phe	Ser	Phe	Leu	Thr
			20					25						30	
Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala	Pro	Pro	Pro	Ser
		35					40					45			
Trp	Asp	Glu	Met	Trp	Lys	Cys	Leu	Val	Arg	Leu	Lys	Pro	Thr	Leu	His
	50					55					60				
Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Pro	Val	Gln	Asn	Glu	Ile
65					70					75					80
Cys	Leu	Thr	His	Pro	Ile	Thr	Lys	Tyr	Ile	Met	Ala	Cys	Met	Ser	
				85				90						95	

(2) INFORMATION FOR SEO ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HD10-1-25

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC GTC ACA AAA TAC ATT ATG	47
Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met	
1 5 10 15	
GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTG TTG	95
Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu	
20 25 30	
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGC	143
Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly	
35 40 45	
TGC GTT GTA ATC GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA CTC	191
Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Leu	
50 55 60	
GTT CCA GAC AAG GAG GTG TTG TAT CAA CAG TAC GAT GAG ATG GAG GAG	239
Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu	
65 70 75	
TGC TCG CAA GCC GCC CCA TAC ATC GAA CAA GCT CAG GTA ATA GCC CAC	287
Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His	
80 85 90 95	
CAG TTC AAG GAG AAA ATC CTT GGA CTG CTG CAG CGA GCC ACC CAA CAA	335
Gln Phe Lys Glu Lys Ile Leu Gly Leu Leu Arg Ala Thr Gln Gln	
100 105 110	
CAA GCT GTC ATT GAG CCC GTA ATA GCT TCC AAC TGG CAA AAG CTT GAA	383
Gln Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu	
115 120 125	
ACC TTC TGG CAC AAG CAT	401
Thr Phe Trp His Lys His	
130	

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met Ala
1 5 10 15

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu
 20 25 30
 Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys
 35 40 45
 Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Leu Val
 50 55 60
 Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys
 65 70 75 80
 Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
 85 90 95
 Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln
 100 105 110
 Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu Thr
 115 120 125
 Phe Trp His Lys His
 130

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 401 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE:

(B) CLONE: HD10-1-3

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TC	CAA	AAT	GAA	ATC	TGC	TTG	ACA	CAC	CCC	GTC	ACA	AAA	TAC	ATT	ATG	47
	Gln	Asn	Glu	Ile	Cys	Leu	Thr	His	Pro	Val	Thr	Lys	Tyr	Ile	Met	
	1					5					10				15	
GCA	TGC	ATG	TCA	GCT	GAT	CTG	GAA	GTA	ACC	ACC	AGC	ACC	TGG	GTG	TTG	95
Ala	Cys	Met	Ser	Ala	Asp	Leu	Glu	Val	Thr	Thr	Ser	Thr	Trp	Val	Leu	
						20					25				30	
CTT	GGA	GGG	GTC	CTC	GCG	GCC	CTA	GCG	GCC	TAC	TGC	TTG	TCA	GTC	GGC	143

Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly	
35 40 45	
TGC GTT GTA ATC GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA CTC	191
Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Leu	
50 55 60	
GTT CCA GAC AAG GAG GTG TTG TAT CAA CAG TAC GAT GAG ATG GAG GAG	239
Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu	
65 70 75	
TGC TCG CAA GCC GCC CCA TAC ATC GAA CAA GCT CAG GTA ATA GCC CAC	287
Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His	
80 85 90 95	
CAG TTC AAG GAG AAA ATC CTT GGA CTG CTG CAG CGA GCC ACC CAA CAA	335
Gln Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln	
100 105 110	
CAA GCT GTC ATT GAG CCC GTA ATA GCT TCC AAC TGG CAA AAG CTT GAA	383
Gln Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu	
115 120 125	
ACC TTC TGG CAC AAG CAT	401
Thr Phe Trp His Lys His	
130	

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met Ala	
1 5 10 15	
Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu	
20 25 30	
Gly Gly Val Leu Ala Ala Leu Ala Tyr Cys Leu Ser Val Gly Cys	
35 40 45	
Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Leu Val	
50 55 60	
Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys	
65 70 75 80	
Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln	
85 90 95	
Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln	

100

105

110

Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu Thr
 115 120 125

Phe Trp His Lys His
 130

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-20-164

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met 1 5 10 15	47
GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu 20 25 30	95
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly 35 40 45	143
TGT GTT GTG ATT GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile 50 55 60	191
GTT CCA GAC AAA GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu 65 70 75	239
TGC TCA CAA GCT GCC CCA TAT ATC GAA CAA GCT CAG GTA ATA GCT CAC Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His 80 85 90 95	287
CAG TTC AAG GGA AAA GTC CIT GGA TTG CTG CAG CGA GCC ACC CAA CAA	335

Gln Phe Lys Gly Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln
 100 105 110

CAA GCT GTC ATT GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG 383
 Gln Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu
 115 120 125

GCC TTT TGG CAC AAG CAT 401
 Ala Phe Trp His Lys His
 130

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala
 1 5 10 15

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu
 20 25 30

Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys
 35 40 45

Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val
 50 55 60

Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys
 65 70 75 80

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
 85 90 95

Phe Lys Gly Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln
 100 105 110

Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala
 115 120 125

Phe Trp His Lys His
 130

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: BR36-20-166

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG	47
Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met	
1 5 10 15	
GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG	95
Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu	
20 25 30	
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT	143
Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly	
35 40 45	
TGT GTT GTG ATT GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC	191
Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile	
50 55 60	
GTT CCA GAC AAA GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG	239
Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu	
65 70 75	
TGC TCA CAA GCT GCC CCA TAT ATC GAA CAA GCT CAG GTG ATA GCT CAC	287
Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His	
80 85 90 95	
CAG TTC AAG GAA AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA	335
Gln Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln	
100 105 110	
CAA GCT GTC ATT GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG	383
Gln Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu	
115 120 125	
GCC TTT TGG CAC AAG CAT	401
Ala Phe Trp His Lys His	
130	

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala
 1             5             10             15
Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu
 20             25             30
Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys
 35             40             45
Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val
 50             55             60
Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys
 65             70             75             80
Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
 85             90             95
Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln
 100            105            110
Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala
 115            120            125
Phe Trp His Lys His
 130

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(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 401 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: BR36-20-165

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG	47
Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met	
1 5 10 15	
GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG	95
Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu	
20 25 30	
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT	143
Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly	
35 40 45	
TGT GTT GTG ATT GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC	191
Cys Val Val Ile Val Gly His Ile Glu Leu Gly Lys Pro Ala Ile	
50 55 60	
GTT CCA GAC AAA GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG	239
Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu	
65 70 75	
TGC TCA CAA GCT GCC CCA TAT ATC GAA CAA GCT CAG GTA ATA GCT CAC	287
Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His	
80 85 90 95	
CAG TTC AAG GAA AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA	335
Gln Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln	
100 105 110	
CAA GCT GTC ATT GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG	383
Gln Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu	
115 120 125	
GCC TTT TGG CAC AAG CAT	401
Ala Phe Trp His Lys His	
130	

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala	
1 5 10 15	
Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu	
20 25 30	
Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys	
35 40 45	

```

Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val
    50                      55                      60

Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys
    65                      70                      75                      80

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
                      85                      90                      95

Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln
    100                      105                      110

Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala
    115                      120                      125

Phe Trp His Lys His
    130

```

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 509 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: PC-2-1
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 3..509
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC      47
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr
    1           5           10           15

AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT      95
Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val
    20           25           30

GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC      143
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg
    35           40           45

GCG ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG      191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln

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50	55	60	
CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC			239
Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro			
65	70	75	
GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG			287
Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly			
80	85	90	95
TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC			335
Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp			
100	105	110	
CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG			383
Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr			
115	120	125	
TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC			431
Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro			
130	135	140	
ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG			479
Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu			
145	150	155	
GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA			509
Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu			
160	165		

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn			
1	5	10	15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly			
20	25	30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala			
35	40	45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro			
50	55	60	
Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly			
65	70	75	80
Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp			

85										90					95				
Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Asn	Trp	Gly	Pro	Asn	Asp	Pro				
100										105					110				
Arg	Arg	Lys	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys				
115										120					125				
Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Gly	Pro	Ile				
130										135					140				
Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp				
145										150					155				
160										165									
Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn	Leu											

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(111) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PC-2-6

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 3..509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CC	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	AAC	ACC	47
Met	Ser	Thr	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	
1					5					10					15	
<hr/>																
AAC	CGT	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	GGT	GGT	CAG	ATC	GTT	95
Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	
				20					25					30		
<hr/>																
GGC	GGA	GIT	TAC	TTG	TTG	CCG	CGC	AGG	GGC	CCT	AGG	ATG	GGT	GTG	CGC	143
Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Met	Gly	Val	Arg	
			35				40						45			
<hr/>																
CGC	ACT	CGG	AAG	ACT	TCG	GAA	CGG	TCG	CAA	CCC	CGT	GGA	CGG	CGT	CAG	191
Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	
		50					55					60				

CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC 239
 Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro
 65 70 75
 GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG 287
 Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly
 80 85 90 95
 TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC 335
 Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp
 100 105 110
 CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG 383
 Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr
 115 120 125
 TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC 431
 Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro
 130 135 140
 ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG 479
 Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu
 145 150 155
 GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA 509
 Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu
 160 165

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15
 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly
 20 25 30
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala
 35 40 45
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60
 Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly
 65 70 75 80
 Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp
 85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile
 130 135 140
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160
 Gly Val Asn Tyr Ala Thr Gly Asn Leu
 165

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 580 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: PC-4-1

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

A	ACG	TGC	GGA	TTC	GCC	GAT	CTC	ATG	GGG	TAT	ATC	CCG	CTC	GTA	GGC	46
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	
	1			5					10					15		
GGC	CCC	ATT	GGG	GGC	GTC	GCA	AGG	GCT	CTC	GCA	CAC	GGT	GTG	AGG	GTC	94
Gly	Pro	Ile	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Val	
			20					25					30			
CTT	GAG	GAC	GGG	GTA	AAC	TAT	GCA	ACA	GGG	AAT	TTA	CCC	GGT	TGC	TCT	142
Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	
			35					40					45			
TTC	TCT	ATC	TTT	ATT	CTT	GCT	CTT	CTC	TCG	TGT	CTG	ACC	GTT	CCG	GCC	190
Phe	Ser	Ile	Phe	Ile	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	
			50					55					60			
TCT	GCA	GTT	CCC	TAC	CGA	AAT	GCC	TCT	GGG	ATT	TAT	CAT	GTT	ACC	AAT	238

Ser	Ala	Val	Pro	Tyr	Arg	Asn	Ala	Ser	Gly	Ile	Tyr	His	Val	Thr	Asn	
65						70					75					
GAT	TGC	CCA	AAC	TCT	TCC	ATA	GTC	TAT	GAG	GCA	GAT	AAC	CTG	ATC	CTA	286
Asp	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asn	Leu	Ile	Leu	
80					85				90				95			
CAC	GCA	CCT	GGT	TGC	GTG	CCT	TGT	GTC	ATG	ACA	GGT	AAT	GTG	AGT	AGA	334
His	Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	Met	Thr	Gly	Asn	Val	Ser	Arg	
			100					105					110			
TGC	TGG	GTC	CAA	ATT	ACC	CCT	ACA	CTG	TCA	GCC	CCG	AGC	CTC	GGA	GCA	382
Cys	Trp	Val	Gln	Ile	Thr	Pro	Thr	Leu	Ser	Ala	Pro	Ser	Leu	Gly	Ala	
			115					120					125			
GTC	ACG	GCT	CCT	CTT	CGG	AGA	GCC	GTT	GAC	TAC	CTA	GCG	GGA	GGG	GCT	430
Val	Thr	Ala	Pro	Leu	Arg	Arg	Ala	Val	Asp	Tyr	Leu	Ala	Gly	Gly	Ala	
			130				135						140			
GCC	CTC	TGC	TCC	GCG	TTA	TAC	GTA	GGA	GAC	GCG	TGT	GGG	GCA	CTA	TTC	478
Ala	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Ala	Cys	Gly	Ala	Leu	Phe	
			145				150					155				
TTG	GTA	GGC	CAA	ATG	TTC	ACC	TAT	AGG	CCT	CGC	CAG	CAC	GCT	ACG	GTG	526
Leu	Val	Gly	Gln	Met	Phe	Thr	Tyr	Arg	Pro	Arg	Gln	His	Ala	Thr	Val	
160					165					170				175		
CAG	AAC	TGC	AAC	TGT	TCC	ATT	TAC	AGT	GGC	CAT	GTT	ACC	GGC	CAC	CGG	574
Gln	Asn	Cys	Asn	Cys	Ser	Ile	Tyr	Ser	Gly	His	Val	Thr	Gly	His	Arg	
				180					185				190			
ATG	GCA															580
Met	Ala															

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Gly	
1				5					10					15		
Pro	Ile	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	
				20				25					30			
Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	
			35				40					45				
Ser	Ile	Phe	Ile	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	
			50				55				60					

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp
65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His
85 90 95

Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys
100 105 110

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val
115 120 125

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala
130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu
145 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
165 170 175

Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met
180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PC-4-6

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

A	ACG	TGC	GGA	TTC	GCC	GAT	CTC	ATG	GGG	TAT	ATC	CCG	CTC	GTA	GGC	46
Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly		
1				5				10					15			
GGC	CCC	ATT	GGG	GGC	GTC	GCA	AGG	GCT	CTC	GCA	CAC	GGT	GTG	AGG	GTC	94

Gly Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val	
20 25 30	
CTT GAG GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA CCC GGT TGC TCT	142
Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser	
35 40 45	
TTC TCT ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC	190
Phe Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala	
50 55 60	
TCT GCA GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT	238
Ser Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn	
65 70 75	
GAT TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA	286
Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu	
80 85 90 95	
CAC GCA CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA	334
His Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg	
100 105 110	
TGC TGG GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GGA GCA	382
Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala	
115 120 125	
GTC ACG GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT	430
Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala	
130 135 140	
GCC CTC TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC	478
Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe	
145 150 155	
TTG GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG	526
Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val	
160 165 170 175	
CAG AAC TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG	574
Gln Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg	
180 185 190	
ATG GCA	580
Met Ala	

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear -

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly
 1 5 10 15
 Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
 20 25 30
 Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45
 Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
 50 55 60
 Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp
 65 70 75 80
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His
 85 90 95
 Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys
 100 105 110
 Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val
 115 120 125
 Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala
 130 135 140
 Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu
 145 150 155 160
 Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
 165 170 175
 Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met
 180 185 190
 Ala

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 959 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: PC-3-4

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC	47
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr	
1 5 10 15	
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT	95
Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val	
20 25 30	
GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC	143
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg	
35 40 45	
GCG ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG	191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln	
50 55 60	
CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC	239
Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro	
65 70 75	
GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG	287
Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly	
80 85 90 95	
TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC	335
Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp	
100 105 110	
CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG	383
Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr	
115 120 125	
TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC	431
Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro	
130 135 140	
ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG	479
Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu	
145 150 155	
GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA CCC GGT TGC TCT TTC TCT	527
Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser	
160 165 170 175	
ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC TCT GCA	575
Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala	
180 185 190	
GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT GAT TGC	623
Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys	
195 200 205	

CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA CAC GCA Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala 210 215 220	671
CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA TGC TGG Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp 225 230 235	719
GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GGA GCA GTC ACG Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr 240 245 250 255	767
GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT GCC CTC Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu 260 265 270	815
TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC TTG GTA Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val 275 280 285	863
GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG CAG AAC Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn 290 295 300	911
TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG ATG GCA Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala 305 310 315	959

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly 20 25 30
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala 35 40 45
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro 50 55 60
Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly 65 70 75 80
Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp 85 90 95

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Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
    100                      105                      110

Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
    115                      120                      125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile
    130                      135                      140

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
    145                      150                      155                      160
Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
    165                      170                      175

Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val
    180                      185                      190

Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro
    195                      200                      205

Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala Pro
    210                      215                      220

Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val
    225                      230                      235                      240

Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala
    245                      250                      255

Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys
    260                      265                      270

Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly
    275                      280                      285

Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys
    290                      295                      300

Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala
    305                      310                      315

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(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 959 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-3-8

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC	47
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr	
1 5 10 15	
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT	95
Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val	
20 25 30	
GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC	143
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg	
35 40 45	
GGC ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG	191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln	
50 55 60	
CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC	239
Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro	
65 70 75	
GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG	287
Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly	
80 85 90 95	
TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC	335
Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp	
100 105 110	
CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG	383
Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr	
115 120 125	
TGC GGA TTC GCC GAT CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC CCC	431
Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro	
130 135 140	
GTT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG	479
Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu	
145 150 155	
GAC GGG GTA AAC TAT CCA ACA GGG AAT TTA CCC GGT TGC TCT TTC TCT	527
Asp Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser	
160 165 170 175	
ATC TTT ATT CTT GCT CTT CTC TCG-TGT CTG ACC GTT CCG GCC TCT GCA	575
Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala	
180 185 190	
GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT GAT TGC	623

Val	Pro	Tyr	Arg	Asn	Ala	Ser	Gly	Ile	Tyr	His	Val	Thr	Asn	Asp	Cys		
			195					200						205			
CCA	AAC	TCT	TCC	ATA	GTC	TAT	GAG	GCA	GAT	AAC	CTG	ATC	CTA	CAC	GCA	671	
Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asn	Leu	Ile	Leu	His	Ala		
		210					215				220						
CCT	GGT	TGC	GTG	CCT	TGT	GTC	ATG	ACA	GGT	AAT	GTG	AGT	AGA	TGC	TGG	719	
Pro	Gly	Cys	Val	Pro	Cys	Val	Met	Thr	Gly	Asn	Val	Ser	Arg	Cys	Trp		
		225				230					235						
GTC	CAA	ATT	ACC	CCT	ACA	CTG	TCA	GCC	CCG	AGC	CTC	GGA	GCA	GTC	ACG	767	
Val	Gln	Ile	Thr	Pro	Thr	Leu	Ser	Ala	Pro	Ser	Leu	Gly	Ala	Val	Thr		
		240			245					250				255			
GCT	CCT	CTT	CGG	AGA	GCC	GTT	GAC	TAC	CTA	GCG	GGA	GGG	GCT	GCC	CTC	815	
Ala	Pro	Leu	Arg	Arg	Ala	Val	Asp	Tyr	Leu	Ala	Gly	Gly	Ala	Ala	Leu		
			260					265					270				
TGC	TCC	GCG	TTA	TAC	GTA	GGA	GAC	GCG	TGT	GGG	GCA	CTA	TTC	TTG	GTA	863	
Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Ala	Cys	Gly	Ala	Leu	Phe	Leu	Val		
		275					280						285				
GGC	CAA	ATG	TTC	ACC	TAT	AGG	CCT	CGC	CAG	CAC	GCT	ACG	GTG	CAG	AAC	911	
Gly	Gln	Met	Phe	Thr	Tyr	Arg	Pro	Arg	Gln	His	Ala	Thr	Val	Gln	Asn		
		290				295					300						
TGC	AAC	TGT	TCC	ATT	TAC	AGT	GGC	CAT	GTT	ACC	GGC	CAC	CGG	ATG	GCA	959	
Cys	Asn	Cys	Ser	Ile	Tyr	Ser	Gly	His	Val	Thr	Gly	His	Arg	Met	Ala		
		305				310					315						

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala
35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp
 85 90 95
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Val
 130 135 140
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160
 Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
 165 170 175
 Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val
 180 185 190
 Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro
 195 200 205
 Asn Ser Ser Ile Val Tyr Gly Ala Asp Asn Leu Ile Leu His Ala Pro
 210 215 220
 Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val
 225 230 235 240
 Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala
 245 250 255
 Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys
 260 265 270
 Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly
 275 280 285
 Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys
 290 295 300
 Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 959 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: PC C/E1

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

CCATGAGCAC GAATCCTAAA CCTCAAGAA AAACCAAAG AAACACCAAC CGTCGCCAC	60
AGGACGTCAA GTTCCCGGGC GGTGGTCAGA TCGTTGGCG AGTTTACTTG TTGCGCGCA	120
GGGGCCCTAG GATGGGTGTG CGCGCGACTC GGAAGACTTC GGAACGGTCG CAACCCCGTG	180
GACGGCGTCA GCCTATTCCC AAGCGCGCGC AGCCACGGG CCGGTCTCTG GGTCAACCCG	240
GGTACCCTTG GCCCCTTAC GCCAATGAGG GCCTCGGGTG GGCAGGGTGG CTGCTCTCCC	300
CTCGAGGCTC TCGGCCTAAT TGGGGCCCCA ATGACCCCG GCGAAAATCG CGTAATTG	360
GTAAGGTCAT CGATACCCTA ACGTSCGGAT TCGCCGATCT CATGGGTAY ATCCCGCTCG	420
TAGGCGGGCC CRTTGGGGGC GTGCAAGGG CTCTCGCACA CGGTGTGAGG GTCTTGAGG	480
ACGGGGTAA CTATSCAACA GGAATTTC CCGGTTGCTC TTTCTCTATC TTTATTCTTG	540
CTCTTCTCTC GTGCTGACC GTTCGGCCT CTGAGTTCC CTACGAAAT GCCTCTGGGA	600
TTTATCATGT TACCAATGAT TGCCCAAAC CTTCATAGT CTATGAGCA GATAACCTGA	660
TCCTACACGC ACCTGGTTGC GTGCCTTGTG TCATGACAGG TAATGTGAGT AGATGCTGGG	720
TCCAAATTAC CCTACACTG TCAGCCCCGA GCCTCGGAGC AGTCAAGGCT CCTCTCGGA	780
GAGCCGTGA CTACCTAGCG GGAGGGGCTG CCCTTGCTC CGCGTTATAC GTAGGAGACG	840
CGTGTGGGC ACTATTCTTG GTAGGCCAAA TGTTACCTA TAGSCCTCG CAGCACGCTA	900
CGGTGCAGAA CTGCAACTGT TCCATTTACA GTGGCCATGT TACCGGCCAC CGGATGGCA	959

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1				5					10				15		

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly
 20 25 30
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala
 35 40 45
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60
 Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly
 65 70 75 80
 Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp
 85 90 95
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Val
 130 135 140
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160
 Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
 165 170 175
 Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val
 180 185 190
 Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro
 195 200 205
 Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala Pro
 210 215 220
 Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val
 225 230 235 240
 Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala
 245 250 255
 Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys
 260 265 270
 Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly
 275 280 285
 Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys
 290 295 300
 Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE:
 (B) CLONE: PC-1-37

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

ACCACCGGAG	CTTCTATCAC	ATACTCCACT	TACGGCAAGT	TCCTTGCTGA	TGGAGGGTGT	60
TCAGCGCGCG	CGCATGACGT	GATCATATGC	GACGAGTGCC	ATTCCACGGA	CGCCACCACC	120
ATTCTTGGGA	TAGGCATGTT	CCTTGACCAG	GCAGAGACGG	CTGGAGCTAG	GCTCGTGTCT	180
TTGGCCACGG	NCAACCCCTC	CGGCAGTGTG	ACAACGCCCC	ACCCCAACAT	CGAGGAAGTG	240
GCCCTGCCTC	AGGAGGGGGA	GGTTCCTTTC	TACGGCAGAG	CCATTCCCTC	TGCTTTTATA	300
AAGGGTGGTA	GGCATCTCAT	CTTCTGCCAT	TCCAAGAAAA	ATTGTGATGA	ACTC	354

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Thr	Thr	Gly	Ala	Ser	Ile	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe	Leu	Ala
1				5					10					15	
Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	His	Asp	Val	Ile	Ile	Cys	Asp	Glu
			20					25					30		

Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr Val Leu
 35 40 45
 Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Xaa
 50 55 60
 Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn Ile Glu Glu Val
 65 70 75 80
 Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Gly Arg Ala Ile Pro
 85 90 95
 Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys
 100 105 110
 Lys Asn Cys Asp Glu Leu
 115

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PC-1-48

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

ACCACCGGAG CTTCATCAC ATACTCCACT TACGGCAAGT TCCTTGCTGA TGGAGGGTGT 60
 TCAGCGCGCG CGTATGACGT GATCATATGC GACGAGTGCC ATTCCCAGGA GCACCACCACC 120
 ATTCCTGGGA TAGGCACTGT CCTTGACCA GCAGAGACGG CTGGAGCTAG GCTCGTCGTC 180
 TTGNCACGG NCACCCCTCC CGGCAGTGTG ACAACGCCCC ACCCCAACAT CAGGAAGTGT 240
 GCCTGCTCTC AGGAGGGGGA GGTTCCTTC TACGGNAGAG CCATTCCCCT TGCTTTTATA 300
 AAGGTTGTTA GGCATCTCAT CTTCTGCCAT TCCAAGAAAA AATGTGATGA ACTT 354

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala
 1             5             10             15

Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val Ile Ile Cys Asp Glu
      20             25             30

Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr Val Leu
      35             40             45

Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Xaa Thr Xaa
      50             55             60

Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn Ile Glu Glu Val
      65             70             75             80

Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Xaa Arg Ala Ile Pro
      85             90             95

Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys
      100             105             110

Lys Lys Cys Asp Glu Leu Arg Gln Ala Thr Asp Gln Pro Gly Arg Glu
      115             120             125

Arg Pro Trp Glu Tyr
      130

```

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) IMMEDIATE SOURCE:

(B) CLONE: PC-1-37

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

ATGGCTTTCA TGTCTCCGGA CTGAGAGGTC ATTACCANCA CTGGGTTCT GGTGGGGGGC      60
GTTGTGGCGA CCCTGNCGNC CTA CTGCTTG ACGGTGGGTT CGGTAGCCAT AGTCGGTAGG      120
ATCATCTCTT CTGGGAACCC TGCCATCATT NCCGATAGGG AGGTATTATA CCAGCAATTT      180
GATGAGATGG AGGAGTGCTC GGCCTCGTTG CCCTATATGG ACGAAACAGC TNCCATTGCC      240
GGACAATTCA AAGAGAAAGT GCTCGGCTTC ATCAGCACGA CCGGCCAGAA GGCTGAAACT      300
CTGAAGCCGG CAGCCACGTC TGTGTGGAAC AAGGCTGATC AGTTCGTGNC CACATAC      357

```

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

```

Met Ala Phe Met Ser Pro Asp Leu Glu Val Ile Thr Xaa Thr Trp Val
 1             5             10             15
Leu Val Gly Gly Val Val Ala Thr Leu Xaa Xaa Tyr Cys Leu Thr Val
          20             25             30
Gly Ser Val Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala
          35             40             45
Ile Ile Xaa Asp Arg Glu Val Leu Tyr Gln Gln Phe Asp Glu Met Glu
 50             55             60
Glu Cys Ser Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Xaa Ile Ala
 65             70             75             80
Gly Gln Phe Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln
          85             90             95
Lys Ala Glu Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala
          100             105             110
Asp Gln Phe Trp Xaa Thr Tyr Met Trp Asn Phe Ile Ser Gly Ile Gln
          115             120             125

```

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: PC-1-48

```
(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 1..357
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

ATGGCTTGCA	TGCTGCGGA	CCTGGAGGT	ATTACCANCA	CTGGGTTCT	GGTGGGGGC	60
GTGTGGCGN	CCCTGGCGC	CTACTGCTT	ACGGTGGGT	CGGTAGCCAT	AGTCGGTAGG	120
ATCATCTCT	CTGGGAAAC	TGCCATCAT	CCCGATAGG	AGGCATTATA	CCNCAATTT	180
GATGAGATG	AGGAGTGTC	GGCCTCGTT	CCCTATATG	ACAGACACG	TGCCATTGCC	240
GGACAATTCA	AAGAGAAAT	GCTCGGCTT	ATCAGCACGA	CCGGCCAGAA	GGCTGAAACT	300
CTGAAGCCG	CAGCCACGT	TGTGTGGA	AAGGCTGANC	AGTTCTGGGC	CACATAC	357

(2) INFORMATION FOR SEQ ID NO: 62:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```

Met Ala Cys Met Ser Ala Asp Leu Glu Val Ile Thr Xaa Thr Trp Val
 1      5      10      15
Leu Val Gly Gly Val Val Ala Xaa Leu Ala Ala Tyr Cys Leu Thr Val
 20      25      30
Gly Ser Val Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala
 35      40      45
Ile Ile Pro Asp Arg Glu Ala Leu Tyr Xaa Gln Phe Asp Glu Met Glu
 50      55      60

```

Glu	Cys	Ser	Ala	Ser	Leu	Pro	Tyr	Met	Asp	Glu	Thr	Arg	Ala	Ile	Ala
65					70				75					80	
Gly	Gln	Phe	Lys	Glu	Lys	Val	Leu	Gly	Phe	Ile	Ser	Thr	Thr	Gly	Gln
			85					90						95	
Lys	Ala	Glu	Thr	Leu	Lys	Pro	Ala	Ala	Thr	Ser	Val	Trp	Asn	Lys	Ala
			100				105						110		
Xaa	Gln	Phe	Trp	Ala	Thr	Tyr	Met	Trp	Asn	Phe	Ile	Ser	Gly	Ile	Gln
			115				120						125		

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCP:161"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

ACCGGAGGCC AGGAGAGTGA TCTCTCTCC

28

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCP:162"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GGGCTGCTCT ATCCTCATCG ACGCCATC

28

(2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPrl63"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GCCAGAGGCT CGGAAGCGCA TCAGCGCT

28

(2) INFORMATION FOR SEQ ID NO: 66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPrl64"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GAGCTGCTCT GTCCTCTCG ACGCCGCA

28

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..28
 (D) OTHER INFORMATION: /standard_name= "HCV Primer
 HCP23"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

CTCATGGGGT ACATTCCGCT

20

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..28
 (D) OTHER INFORMATION: /standard_name= "HCV Primer
 HCP54"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

CTATTACCAG TTCATCATCA TATCCCA

27

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPrl16"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

TTTTAAATAC ATCATGRCTG YATG

24

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPrl66"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CTATTATTGT ATCCCRCTGA TGAARTTCCA CAT

33

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..28
(D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPrl18:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

ACTAGTCGAC TAYTGATCCR CTATRWARTT CCACAT

36

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..28
(D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPrl17:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

TTTTAAATAC ATGCRCTGC ATGCA

25

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..28
(D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPrl19:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

ACTAGTCGAC TARTTGCATA GCCKRTTCAT CCAYTG

36

(2) INFORMATION FOR SEQ ID NO: 74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: YES

- (iii) ANTI-SENSE: NO

- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPrl31:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

GGAATTCTAG ACCTCTGGGA YGARAYTGA ARTG

34

(2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: YES

- (iii) ANTI-SENSE: NO

- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPrl30:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

GGAATTCTAG ACGCTAYCAR GCACGTTGYG C

31

(2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPrl34:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CATATAGATG CCCACTTCCT ATC

23

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iii) ANTI-SENSE: YES
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPrl3:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GTGTGCCAGG ACCATC

16

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPPr4:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

GACATGCATG TCATGATGTA

20

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPPr152:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TACGCTCTT CTATATCGGT TGGGGCTG

29

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPPr52:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

ATGTTGGGTA AGGTCATCGA TACCCT

26

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPPr41:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CCCGGGAGGT CTCGTAGACC GTGCA

25

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPPr40:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

CTATTAAAGA TAGAGAAAGA GCAACCGGG

29

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 192 to 203 of the V1 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 192 to 203 of the V1 region of HCV
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(iii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 213 to 223 of the V2 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Val	Tyr	Glu	Ala	Asp	Asp	Val	Ile	Leu	His	Thr
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 213 to 233 of the V2 region of HCV
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Val	Tyr	Glu	Ala	Asp	Asn	Leu	Ile	Leu	His	Ala
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 242 of the V3 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Val Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 242 of the V3 region of HCV
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Val Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 248 to 257 of the V4 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Val Arg Tyr Val Gly Ala Thr Thr Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 248 to 257 of the V4 region of HCV
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Ala Pro Ser Leu Gly Ala Val Thr Ala Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 294 to 303 of the V5 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Arg Pro Arg Arg His Gln Thr Val Gln Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 294 to 303 of the V5 region of HCV
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Arg Pro Arg Gln His Ala Thr Val Gln Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 70 to 78 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Gln Pro Thr Gly Arg Ser Trp Gly Gln
1 5

(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR33 and BR36

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 237 of the V3 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

Val Gln Asp Gly Asn Thr Ser Thr
1 5

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HD10

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 237 of the V3 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

Val Gln Asp Gly Asn Thr Ser Ala
1 5

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR36

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 248 to 257 of the V4 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

Val Lys Tyr Val Gly Ala Thr Thr Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR36

(viii) POSITION IN GENOME:

(B) MAP POSITION: Positions 1688 to 1707 of HCV type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

Leu	Gly	Gly	Lys	Pro	Ala	Ile	Val	Pro	Asp	Lys	Glu	Val	Leu	Tyr	Gln
1				5				10				15			
Gln Tyr Asp Glu															
20															

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HD10

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1688 to 1707 of HCV type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

Leu	Gly	Gly	Lys	Pro	Ala	Leu	Val	Pro	Asp	Lys	Glu	Val	Leu	Tyr	Gln
1				5				10				15			
Gln Tyr Asp Glu															
20															

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1712 to 1731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
1 5 10 15

Phe Lys Glu Lys
20

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR36

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1724 to 1743 of HCV type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

Ile Ala His Gln Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala
1 5 10 15

Thr Gln Gln Gln
20

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HD10

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1724 to 1743 of HCV type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

Ile Ala His Gln Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala
1 5 10 15

Thr Gln Gln Gln
20

(2) INFORMATION FOR SEQ ID NO: 102:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1688 to 1707 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Ala Leu Tyr Gln
1 5 10 15

Gln Phe Asp Glu
20

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1688 to 1707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Val Leu Tyr Gln
1 5 10 15

Gln Phe Asp Glu
20

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: position 1712 to 1731 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

Ser	Ala	Ser	Leu	Pro	Tyr	Met	Asp	Glu	Thr	Arg	Ala	Ile	Ala	Gly	Gln
1				5					10					15	
Phe	Lys	Glu	Lys												
				20											

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1724 to 1743 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

Ile	Ala	Gly	Gln	Phe	Lys	Glu	Lys	Val	Leu	Gly	Phe	Ile	Ser	Thr	Thr
1				5					10					15	
Gly	Gln	Lys	Ala												
				20											

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB48-3-10

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

C TCC ACT GTA ACC GAA AAG GAC ATC AGG GTC GAG GAG GAG GTC TAT	46
Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAC CTG GAG CCC GAA GCC CGC AAG GCA ATT ACC GCC CTA	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Thr Ala Leu	
20 25 30	
ACA GAG AGA CTC TAC GTG GGC GGT CCC ATG CAT AAC AGC AAG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp	
35 40 45	
CTG TGC GGG TAT CGC AGA TGT CGC GCA AGC GGC GTC TAC ACC ACC AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACA CTG ACG TGC TAC CTC AAA GCC TCA GCC GCT ATC AAA	238
Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Lys	
65 70 75	
GCG GCG GGG CTG AGA GAC TGC ACC ATG TTG GTC TGT GGT GAT GAC CTG	286
Ala Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTT GTC ATC GCT GAG AGC GAT GGC GTA GAG GAG GAC AAA CGA CCC CTC	334
Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Pro Leu	
100 105 110	
GGA GCC	340
Gly Ala	

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln
1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Thr Ala Leu Thr
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Lys Ala
65 70 75 80

Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Pro Leu Gly
100 105 110

Ala

(2) INFORMATION FOR SEO ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB116-3-5

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 108:

C	TCC	ACT	GTA	ACC	GAA	AAG	GAC	ATC	AGG	GTC	GAG	GAG	GAG	GTA	TAT	46
Ser	Thr	Val	Thr	Glu	Lys	Asp	Ile	Arg	Val	Glu	Glu	Glu	Val	Tyr		
	1				5				10					15		
<hr/>																
CAG	TGT	TGT	GAC	CTG	GAG	CCC	GAG	GCC	CGC	AGA	GCA	ATT	ACC	GCC	CTA	94
Gln	Cys	Cys	Asp	Leu	Glu	Pro	Glu	Ala	Arg	Arg	Ala	Ile	Thr	Ala	Leu	
				20					25					30		
<hr/>																
ACA	GAG	AGA	CTC	TAC	GTG	GGC	GGT	CCC	ATG	CAT	AAC	AGC	AGG	GGA	GAC	142
Thr	Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Met	His	Asn	Ser	Arg	Gly	Asp	
			35				40					45				

CTG TGC GGG TAT CGC AGA TGC CGT GCG AGC GGC GTC TAC ACC ACC AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACA CTG ACG TGC TAT CTC AAA GCC TCA GCC GCT ATC AGA	238
Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg	
65 70 75	
GCG GCG GGG CTG AGA GAC TGC ACC ATG TTG GTC TGT GGT GAT GAC CTG	286
Ala Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTC GTC ATT GCT GAA AGC GAT GGC GTA GAG GAG GAC AAA CGA GCC CTC	334
Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu	
100 105 110	
GGA GCC	340
Gly Ala	

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln	
1 5 10 15	
Cys Cys Asp Leu Glu Pro Glu Ala Arg Arg Ala Ile Thr Ala Leu Thr	
20 25 30	
Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Arg Gly Asp Leu	
35 40 45	
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe	
50 55 60	
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala	
65 70 75 80	
Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val	
85 90 95	
Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu Gly	
100 105 110	
Ala	

(2) INFORMATION FOR SEQ ID NO: 110:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 (B) CLONE: GB215-3-8
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..340
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:
- | | |
|---|-----|
| C TCC ACT GTA ACC GAA AAA GAC ATC AGG GTC GAG GAG GAG GTA TAT | 46 |
| Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr | |
| 1 5 10 15 | |
| CAG TGT TGT GAC CTG GAG CCC GAA GCC CGC AAG GTA ATT ACC GCC CTA | 94 |
| Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu | |
| 20 25 30 | |
| ACA GAG AGA CTC TAT GTG GGC GGT CCC ATG CAT AAT AGC AAA GGA GAC | 142 |
| Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp | |
| 35 40 45 | |
| CTG TGC GGG TAT CGC AGA TGC CGC GCA AGC GGC GTC TAC ACC ACC AGC | 190 |
| Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser | |
| 50 55 60 | |
| TTC GGG AAC ACA CTG ACG TGC TAT CTC AAA GCC TCA GCC GCC ATC AGG | 238 |
| Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg | |
| 65 70 75 | |
| GCG TCA GGG CTG AGA GAC TGC ACT ATG CTG GTC TAT GGT GAC GAC CTG | 286 |
| Ala Ser Gly Leu Arg Asp Cys Thr Met Leu Val Tyr Gly Asp Asp Leu | |
| 80 85 90 95 | |
| GTC GTC ATT GCC GAG AGC GAT GGC GTA GAG GAG GAC AAA CGA GCC CTC | 334 |
| Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu | |
| 100 105 110 | |
| GGA GTC | 340 |
| Gly Val | |
- (2) INFORMATION FOR SEQ ID NO: 111:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```
Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln
 1             5             10             15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr
 20             25             30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
 35             40             45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
 50             55             60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala
 65             70             75             80

Ser Gly Leu Arg Asp Cys Thr Met Leu Val Tyr Gly Asp Asp Leu Val
 85             90             95

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
 100            105            110

Val
```

(2) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: GB358-3-3

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

C TCC ACT GTA ACC GAA AAG GAC ATC AGG GTC GAG GAG GAG GTG TAT

46

Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 114:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB549-3-6

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

C TCC ACG GTG ACC GAA AGG GAT ATC AGG ACC GAG GAA GAG ATC TAC Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ile Tyr 1 5 10 15	46
CAG TGC TGC GAC CTG GAG CCC GAA GCC CGC AAG GTG ATA TCC GCC CTA Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu 20 25 30	94
ACG GAA AGA CTC TAC GTG GGC GGT CCC ATG TAC AAC TCC AAG GGG GAC Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp 35 40 45	142
CTA TGC GGG CAA CGG AGG TGC CGC GCA AGC GGG GTC TAC ACC ACC AGC Leu Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser 50 55 60	190
TTC GGG AAC ACT GTA ACG TGT TAT CTC AAG GCC GTT GCG GCT ACT AGG Phe Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg 65 70 75	238
GCC GCA GGT CTG AAA GGT TGC AGC ATG CTG GTT TGT GGA GAC GAC TTA Ala Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu 80 85 90 95	286

GTC GTC ATC TGC GAG AGC GGC GGC GTA GAG GAG GAT GCA AGA GCC CTC 334
 Val Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu
 100 105 110

CGA GCC 340
 Arg Ala

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr Gln
 1 5 10 15
 Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu Thr
 20 25 30
 Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu
 35 40 45
 Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
 50 55 60
 Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg Ala
 65 70 75 80
 Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95
 Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu Arg
 100 105 110
 Ala

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB809-3-1

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

C TCC ACT GTG ACT GAG AGA GAC ATC AAG GTC GAA GAA GAA GTC TAT	46
Ser Thr Val Thr Glu Arg Asp Ile Lys Val Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAT CTG GAG CCC GAG GCC CGC AAG GTA ATA GCC GCC CTC	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ala Ala Leu	
20 25 30	
ACG GAG AGA CTC TAC GTG GGC GGC CCC ATG CAT AAC AGC AAG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp	
35 40 45	
CTT TGC GGG TAT CGT AGA TGC CGC GCG AGC GGC GTA TAC ACC ACC AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACA ATG ACG TGC TAC CTT AAG GCC TCA GCA GCC ATC AGG	238
Phe Gly Asn Thr Met Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg	
65 70 75	
GCT GCG GGG CTA AAG GAT TGC ACC ATG CTG GTT TGC GGT GAC GAC CTA	286
Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTC GTG ATC GCC GAG AGC GGT GGC GTT GAG GAG GAC AAA CGA GCC CTC	334
Val Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu	
100 105 110	
GGA GCT	340
Gly Ala	

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

Ser Thr Val Thr Glu Arg Asp Ile Lys Val Glu Glu Glu Val Tyr Gln
1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ala Ala Leu Thr
 20 25 30
 Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
 35 40 45
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
 50 55 60
 Gly Asn Thr Met Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala
 65 70 75 80
 Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95
 Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
 100 105 110
 Ala

(2) INFORMATION FOR SEQ ID NO: 118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 574 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: GB358-4-1
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCT GTG GGT GGC GTC GCC AGG GCC CTG GCA CAC GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGG ATC AAT TAT TCG ACA GGG AAT CTT CCC GGT TGC TCT TTC	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	

TCT ATC TTC CTC TTG GCA CTT CTT TCG TGC CTG ACT GTT CCC ACC TCG	192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	
50 55 60	
GCC GTC AAC TAT CGC AAT GCC TCG GGC ATC TAT CAC ATC ACC AAT GAC	240
Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp	
65 70 75 80	
TGC CCG AAC TCG AGC ATA GTG TAC GAG ACC GAG CAC CAC ATC CTA CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Ile Leu His	
85 90 95	
CTC CCA GGG TGT TTA CCC TGC GTG AGG GTT GGG AAT CAG TCA CGC TGC	336
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTG GCC CTC ACT CCC ACC GTG GCG GCG CCT TAC ATC GGC GCT CCG	384
Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro	
115 120 125	
CTT GAA TCC CTC CGG AGT CAT GTG GAT CTG ATG GTA GGT GCC GCT ACT	432
Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr	
130 135 140	
GCG TGC TCC GCT CTT TAC ATC GGA GAC CTG TGC GGT GGC GTA TTC TTG	480
Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu	
145 150 155 160	
GTT GGT CAG ATG TTC TCT TTC CAG CCG CGG CGC CAC TGG ACT ACG CAG	528
Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln	
165 170 175	
GAC TGC AAT TGT TCC ATC TAC GCG GGG CAC GTT ACG GGC CAC AGG A	574
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg	
180 185 190	

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
20 25 30
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser

50	55	60
Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp		
65	70	75 80
Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Ile Leu His		
	85	90 95
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys		
	100	105 110
Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro		
	115	120 125
Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr		
	130	135 140
Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu		
	145	150 155 160
Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln		
	165	170 175
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg		
	180	185 190

(2) INFORMATION FOR SEQ ID NO: 120:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 574 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB549-4-3

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

ACG TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCT GTG GGT GGC GTC GCC AGG GCC TTG GCA CAT GGT GTC AGG GCC GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	

GAG GAC GGG ATT AAC TAT GCA ACA GGG AAT CTT CCC GGT TGC TCC TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTT CTA GCA CTT CTC TCG TGC TTG ACT GTC CCG GCC TCG	192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
CGC CAG CAC TAC CGG AAC ATC TCG GGC ATT TAT CAC GTC ACC AAT GAC	240
Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp	
65 70 75 80	
TGC CCG AAC TCT AGT ATA GTG TAT GAA GCT GAC CAT CAT ATC ATG CAT	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His	
85 90 95	
CTA CCA GGG TGT GTG CCT TGC GTG AGA ACC GGG AAC ACC TCG CGC TGC	336
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys	
100 105 110	
TGG GTT CCT TTA ACA CCC ACT GTG GCT GCC CCC TAT GTT GGC GCG CCG	384
Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro	
115 120 125	
CTC GAA TCC ATG CGG CGS CAC GTG GAC TTA ATG GTG GGT GCC GCC ACC	432
Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr	
130 135 140	
GTC TGC TCG GCC CTG TAC ATC GGA GAC CTT TGC GGA GGT GTC TTC CTG	480
Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu	
145 150 155 160	
GTC GGG CAG ATG TTC ACC TTC CGG CCG CGC CGC CAT TGG ACT ACC CAG	528
Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln	
165 170 175	
GAC TGC AAC TGC TCT ATC TAT GAT GGC CAC ATC ACC GGC CAT AGA A	574
Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg	
180 185 190	

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
 50 55 60
 Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp
 65 70 75 80
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His
 85 90 95
 Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys
 100 105 110
 Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro
 115 120 125
 Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
 130 135 140
 Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu
 145 150 155 160
 Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln
 165 170 175
 Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg
 180 185 190

(2) INFORMATION FOR SEQ ID NO: 122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 574 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: GB809-4-3
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..574
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

ACG TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC

48

Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	
1				5					10					15		
CCC	GTT	GGG	GGC	GTC	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	AGG	GCT	GTG	96
Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Ala	Val	
				20				25					30			
GAG	GAC	GGG	ATT	AAC	TAT	GCG	ACA	GGG	AAT	CTT	CCC	GGT	TGC	TCT	TTC	144
Glu	Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	
			35				40					45				
TCT	ATC	TTC	CTC	CTG	GCA	CTT	CTT	TCG	TGC	CTC	ACT	GTC	CCA	GCG	TCA	192
Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	
			50			55					60					
GCT	GAG	CAC	TAC	CGG	AAT	GCT	TCG	GGC	ATC	TAT	CAC	ATC	ACC	AAT	GAC	240
Ala	Glu	His	Tyr	Arg	Asn	Ala	Ser	Gly	Ile	Tyr	His	Ile	Thr	Asn	Asp	
				70					75					80		
TGT	CCG	AAT	TCC	AGC	GTA	GTC	TAT	GAA	ACT	GAC	CAC	CAT	ATA	TTG	CAC	288
Cys	Pro	Asn	Ser	Ser	Val	Val	Tyr	Glu	Thr	Asp	His	His	Ile	Leu	His	
				85					90					95		
TTG	CCG	GGG	TGC	GTA	CCC	TGC	GTG	AGG	GCC	GGG	AAC	GTG	TCT	CGT	TGC	336
Val	Pro	Gly	Cys	Val	Pro	Gly	Ala	Gly	Ala	Gly	Asn	Val	Ser	Arg	Cys	
				100				105				110				
TGG	ACG	CCG	GTA	ACA	CCT	ACG	GTG	GCT	GCC	GTA	TCC	ATG	GAC	GCT	CCG	384
Trp	Thr	Pro	Val	Thr	Pro	Thr	Val	Ala	Ala	Val	Ser	Met	Asp	Ala	Pro	
			115				120					125				
CTC	GAG	TCC	TTC	CGG	CGG	CAT	GTG	GAC	CTA	ATG	GTA	GGT	GCG	GCC	ACC	432
Leu	Glu	Ser	Phe	Arg	Arg	His	Val	Asp	Leu	Met	Val	Gly	Gly	Ala	Thr	
			130			135					140					
GTG	TGT	TCT	GTC	CTC	TAT	GTT	GGA	GAC	CTC	TGT	GGA	GGT	GCT	TTC	CTA	480
Val	Cys	Ser	Val	Leu	Tyr	Val	Gly	Asp	Leu	Cys	Gly	Gly	Ala	Phe	Leu	
	145			150					155					160		
GTG	GGG	CAG	ATG	TTC	ACC	TTC	CAG	CCG	CGT	GCG	CAC	TGG	ACC	ACG	CAG	528
Val	Gly	Gln	Met	Phe	Thr	Phe	Gln	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln	
				165					170				175			
GAT	TGT	AAT	TGC	TCC	ATC	TAT	ACT	GGC	CAT	ATC	ACC	GGC	CAC	AGG	A	574
Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Thr	Gly	His	Ile	Thr	Gly	His	Arg		
			180					185				190				

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1           5           10          15
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
          20          25          30
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
          35          40          45
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
          50          55          60
Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp
 65          70          75          80
Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His
          85          90          95
Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys
          100         105         110
Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro
          115         120         125
Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
          130         135         140
Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu
          145         150         155         160
Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln
          165         170         175
Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg
          180         185         190

```

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCP206"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

TGGGGATCCC GTATGATACC CGCTGCTTTG A

31

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HcPr207"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

GCGCGAATTC CTGGTCATAG CCTCCGTGAA

30

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Amino acid
- (C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

Gln	His	Tyr	Arg	Asn	Ile	Ser	Gly	Ile	Tyr	His	Val
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Amino acid
- (C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

Glu	His	Tyr	Arg	Asn	Ala	Ser	Gly	Ile	Tyr	His	Ile
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

Val	Tyr	Glu	Thr	Glu	His	His	Ile	Leu	His	Leu
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 130:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

Val Tyr Glu Ala Asp His His Ile Met His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 131:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Val Tyr Glu Thr Asp His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 132:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Val Arg Val Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

Val Arg Thr Gly Asn Thr Ser Arg Cys Trp Val Pro Leu
1 5 10

(2) INFORMATION FOR SEO ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

Val Arg Ala Gly Asn Val Ser Arg Cys Trp Thr Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB358
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:
- | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Pro | Tyr | Ile | Gly | Ala | Pro | Leu | Glu | Ser |
| 1 | | | | 5 | | | | | 10 |
- (2) INFORMATION FOR SEQ ID NO: 136:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB549
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:
- | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Pro | Tyr | Val | Gly | Ala | Pro | Leu | Glu | Ser |
| 1 | | | | 5 | | | | | 10 |
- (2) INFORMATION FOR SEQ ID NO: 137:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB809
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:
- | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Val | Ser | Met | Asp | Ala | Pro | Leu | Glu | Ser |
| 1 | | | | 5 | | | | | 10 |
- (2) INFORMATION FOR SEQ ID NO: 138:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB358 and GB809
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:
- | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Pro | Arg | Arg | His | Trp | Thr | Thr | Gln | Asp |
| 1 | | | | 5 | | | | | 10 |

- (2) INFORMATION FOR SEQ ID NO: 139:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB549
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:
- | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Pro | Arg | Arg | His | Trp | Thr | Thr | Gln | Asp |
| 1 | | | | 5 | | | | | 10 |

- (2) INFORMATION FOR SEQ ID NO: 140:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

Arg Pro Arg Arg His Trp Thr Thr Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 141:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TGGGATATGA TGAATGAATG GTC

23

(2) INFORMATION FOR SEQ ID NO: 142:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

CCAGGTACAA CCGAACCAAT TGCC

24

(2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 957 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..957

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACT AAC	48
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGC CAG ATC GTT GGT	96
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
GGA GTA TAC TTG TTG CCG CGC AGG GGC CCC CGG TTG GGT GTG CGC GCG	144
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
ACG AGG AAA ACT TCC GAG CGG TCC CAG CCA CGT GGG AGG CGC CAG CCC	192
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
ATC CCC AAA GAT CGG CGC CCC ACT GGC AAG TCC TGG GGA AAA CCA GGA	240
Ile Pro Lys Asp Arg Arg Pro Thr Gly Lys Ser Trp Gly Lys Pro Gly	
65 70 75 80	
TAC CCT TGG CCC CTG TAC GGG AAT GAG GGC CTC GGC TGG GCA GGG TGG	288
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp	
85 90 95	
CTC CTG TCC CCC CGA GGG TCT CGC CCG TCA TGG GGC CCA ACT GAC CCC	336
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro	
100 105 110	
CGG CAC AGG TCA CGC AAC TTG GGT AAG GTC ATC GAT ACC CTT ACG TGT	384
Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys	
115 120 125	
GGC TTT GCC GAC CTC ATG GGG TAC ATC CCT GTC GTC GGC GCC CCA GTT	432
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Val	
130 135 140	
GGT GGT GTC GCC AGA GCT CTC GCG CAT GGC GTG AGA GTT CTG GAA GAC	480
Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp	
145 150 155 160	

GGG ATA AAC TAT GCA ACA GGG AAC TTG CCC GGT TGC TCC TTT TCT ATC Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile 165 170 175	528
TTC TTA TTG GCC CTG CTA TCT TGT ATC ACT GTG CCG GTC TCC GGC TTG Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Gly Leu 180 185 190	576
CAG GTC AAG AAC ACC AGC AGC TCT TAC ATG GTA ACC ART GAC TGC CAG Gln Val Lys Asn Thr Ser Ser Tyr Met Val Thr Asn Asp Cys Gln 195 200 205	624
AAC AGT AGC ATC GTC TGG CAG CTC AGG GAT GCT GTT CTT CAC GTC CCC Asn Ser Ser Ile Val Trp Gln Leu Arg Asp Ala Val Leu His Val Pro 210 215 220	672
GGG TGT GTC CCT TGT GAG GAG AAG GGC AAC ATA TCC CGC TGT TGG ATA Gly Cys Val Pro Cys Glu Glu Lys Gly Asn Ile Ser Arg Cys Trp Ile 225 230 235 240	720
CCG GTT TCG CCC AAT ATA GCT GTG AGC CAA CCT GGT GCG CTT ACC AAG Pro Val Ser Pro Asn Ile Ala Val Ser Gln Pro Gly Ala Leu Thr Lys 245 250 255	768
GGC CTG CGG ACG CAT ATT GAT ACC ATC ATT GCA TCC GCT ACG TTT TGC Gly Leu Arg Thr His Ile Asp Thr Ile Ile Ala Ser Ala Thr Phe Cys 260 265 270	816
TCT GCC CTG TAC ATA GGA GAC CTG TGT GGC GCG GTG ATG TTG GCT TCT Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Ala Val Met Leu Ala Ser 275 280 285	864
CAA GTC TTC ATC ATC TCG CCC CAG CAT CAT AAG TTT GTC CAG GAC TGC Gln Val Phe Ile Ile Ser Pro Gln His His Lys Phe Val Gln Asp Cys 290 295 300	912
AAC TGT TCC ATA TAC CCA GGC CAC ATC ACT GGA CAT CGG ATG GCG Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala 305 310 315	957

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
 35 40 45
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60
 Ile Pro Lys Asp Arg Arg Pro Thr Gly Lys Ser Trp Gly Lys Pro Gly
 65 70 75 80
 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp
 85 90 95
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Val
 130 135 140
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160
 Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
 165 170 175
 Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Gly Leu
 180 185 190
 Gln Val Lys Asn Thr Ser Ser Ser Tyr Met Val Thr Asn Asp Cys Gln
 195 200 205
 Asn Ser Ser Ile Val Trp Gln Leu Arg Asp Ala Val Leu His Val Pro
 210 215 220
 Gly Cys Val Pro Cys Glu Glu Lys Gly Asn Ile Ser Arg Cys Trp Ile
 225 230 235 240
 Pro Val Ser Pro Asn Ile Ala Val Ser Gln Pro Gly Ala Leu Thr Lys
 245 250 255
 Gly Leu Arg Thr His Ile Asp Thr Ile Ile Ala Ser Ala Thr Phe Cys
 260 265 270
 Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Ala Val Met Leu Ala Ser
 275 280 285
 Gln Val Phe Ile Ile Ser Pro Gln His His Lys Phe Val Gln Asp Cys
 290 295 300
 Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 2..337

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

C TCA ACG GTC ACG GAG AGG GAC ATC AGA ACT GAG GAG TCC ATA TAC	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr	
1 5 10 15	
CTT GCT TGC TCT TTA CCC GAG CAG GCA CGG ACT GCC ATA CAC TCA CTG	94
Leu Ala Cys Ser Leu Pro Glu Gln Ala Thr Ala Ile His Ser Leu	
20 25 30	
ACT GAG AGG CTT TAC GTG GGA GGG CCC ATG CTA AAC AGC AAA GGG CAA	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Leu Asn Ser Lys Gly Gln	
35 40 45	
ACC TGC GGA TAC AGA CGC TGC CGC GCC AGC GGA GTG TTC ACC ACT AGC	190
Thr Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser	
50 55 60	
ATG GGA AAT ACC ATC ACG TGC TAC GTG AAG GCA CAA GCA GCC TGT AAG	238
Met Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Gln Ala Ala Cys Lys	
65 70 75	
GCT GCG GGC ATA ATT GCC CCC ACG ATG CTG GTG TGC GGC GAC GAT CTA	286
Ala Ala Gly Ile Ile Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTT GTC ATC TCA GAG AGT CAG GGG ACC GAG GAG GAC GAG CGG AAC CTA	334
Val Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu	
100 105 110	
CGA GCC	340
Arg Ala	

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

```

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu
 1             5             10             15
Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr
          20             25             30
Glu Arg Leu Tyr Val Gly Gly Pro Met Leu Asn Ser Lys Gly Gln Thr
          35             40             45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met
          50             55             60
Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Gln Ala Ala Cys Lys Ala
          65             70             75             80
Ala Gly Ile Ile Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
          85             90             95
Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu Arg
          100             105             110

```

Ala

(2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..345

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

ATG AGC ACA CTT CCT AAA CCA CAA AGA AAA ACC AAA AGA AAC ACC AAC

48

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
CCC GGC CAC AGG ACG TTA AGT TCC CAG GCG GCG GTC AGA TCG TTG GTG	96
Pro Gly His Arg Thr Leu Ser Ser Gln Ala Ala Val Arg Ser Leu Val	
20 25 30	
GAG TTT ACG TGC TAC CAC GCA GGG GCC CCC AGT TGG GTG TGC GTG CAG	144
Glu Phe Thr Cys Tyr His Ala Gly Ala Pro Ser Trp Val Cys Val Gln	
35 40 45	
TGC GCA AGA CTT CCG AGC GGT CGC AAC CTC GCA GTA GGC GCC AAC CCA	192
Cys Ala Arg Leu Pro Ser Gly Arg Asn Leu Ala Val Gly Ala Asn Pro	
50 55 60	
TCC CCA GGG CGC GCC GAA CCG AGG GCA GGT CCT GGG CTC AGC CCG GGT	240
Ser Pro Gly Arg Ala Glu Pro Arg Ala Gly Pro Gly Leu Ser Pro Gly	
65 70 75 80	
ACC CTT GGC CCC TAT ATG GGA ATG AGG GCT GCG GGT GGG CAG GGT GGC	288
Thr Leu Gly Pro Tyr Met Gly Met Arg Ala Ala Gly Gly Gln Gly Gly	
85 90 95	
TCC TGT CCC CGC GCG GCT CTC GCC CGT CGT GGG GCC CAA ATG ACC CCC	336
Ser Cys Pro Arg Ala Ala Leu Ala Arg Gly Ala Gln Met Thr Pro	
100 105 110	
GGC GCA GGA	345
Gly Ala Gly	
115	

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
Pro Gly His Arg Thr Leu Ser Ser Gln Ala Ala Val Arg Ser Leu Val	
20 25 30	
Glu Phe Thr Cys Tyr His Ala Gly Ala Pro Ser Trp Val Cys Val Gln	
35 40 45	
Cys Ala Arg Leu Pro Ser Gly Arg Asn Leu Ala Val Gly Ala Asn Pro	
50 55 60	
Ser Pro Gly Arg Ala Glu Pro Arg Ala Gly Pro Gly Leu Ser Pro Gly	
65 70 75 80	
Thr Leu Gly Pro Tyr Met Gly Met Arg Ala Ala Gly Gly Gln Gly Gly	

85

90

95

Ser Cys Pro Arg Ala Ala Leu Ala Arg Arg Gly Ala Gln Met Thr Pro
 100 105 110

Gly Ala Gly
 115

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..280

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

G GCC TGT GAC CTC AAG GAC GAG GCT AGG AGG GTG ATA ACT TCA CTC	46
Ala Cys Asp Leu Lys Asp Glu Ala Arg Arg Val Ile Thr Ser Leu	
1 5 10 15	
ACG GAG CGG CTT TAC TGT GGT GGT CCT ATG TTC AAC AGC AAG GGA CAA	94
Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Gln	
20 25 30	
CAC TGC GGT TAC CGC CGC TGC CGT GCT AGT GGG GTG CTA CCC ACC AGC	142
His Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser	
35 40 45	
TTC GGG AAC ACA ATC ACC TGT TAC ATC AAA GCA AAG GCA GCT ACC AAA	190
Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Lys Ala Thr Lys	
50 55 60	
GCT GCC GGA ATT AAA AAT CCA TCA TTC CTT GTC TGC GGA GAT GAC TTG	238
Ala Ala Gly Ile Lys Asn Pro Ser Phe Leu Val Cys Gly Asp Asp Leu	
65 70 75	
GTC GTG ATT GCT GAG AGT GCA GGG ATC GAT GAG GAC AGA GCG	280
Val Val Ile Ala Glu Ser Ala Gly Ile Asp Glu Asp Arg Ala	
80 85 90	

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

```

Ala Cys Asp Leu Lys Asp Glu Ala Arg Arg Val Ile Thr Ser Leu Thr
 1             5             10             15

Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Gln His
          20             25             30

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Phe
          35             40             45

Glu Asn Thr Ile Thr Cys Tyr Ile Lys Ala Lys Ala Ala Thr Lys Ala
          50             55             60

Ala Gly Ile Lys Asn Pro Ser Phe Leu Val Cys Gly Asp Asp Leu Val
          65             70             75             80

Val Ile Ala Glu Ser Ala Gly Ile Asp Glu Asp Arg Ala
          85             90

```

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 499 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..499

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

```

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC AAC      48
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1             5             10             15

CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGC      96
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
          20             25             30

```

GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC GCG 144
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala
 35 40 45

ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG CCT 192
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60

ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC GGG 240
 Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly
 65 70 75 80

TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG TGG 288
 Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp
 85 90 95

CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC CCC 336
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110

CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG TGC 384
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125

GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC ATT 432
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile
 130 135 140

GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG GAC 480
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160

GGG GTA AAC TAT GCA ACA G 499
 Gly Val Asn Tyr Ala Thr
 165

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly
 20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala
 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60
 Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly
 65 70 75 80
 Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp
 85 90 95
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile
 130 135 140
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160
 Gly Val Asn Tyr Ala Thr
 165

(2) INFORMATION FOR SEQ ID NO: 153:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

ACG TGC GGA TTC GCC GAT CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly	
1 5 10 15	
CCC GTT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu	
20 25 30	
GAG GAC GGG GTA AAC TAT CCA ACA GGG AAT TTA CCC GGT TGC TCT TTC	144

Glu Asp Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC TCT	192
Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCA GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT GAT	240
Ala Val, Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp	
65 70 75 80	
TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His	
85 90 95	
GCA CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA TGC	336
Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys	
100 105 110	
TGG GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GGA GCA GTC	384
Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val	
115 120 125	
ACG GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT GCC	432
Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala	
130 135 140	
CTC TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC TTG	480
Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu	
145 150 155 160	
GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG CAG	528
Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln	
165 170 175	
AAC TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG ATG	576
Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met	
180 185 190	
GCG	579
Ala	

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
 20 25 30

Glu Asp Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45

Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
 50 55 60

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp
 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His
 85 90 95

Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys
 100 105 110

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val
 115 120 125

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala
 130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu
 145 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
 165 170 175

Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 155:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 579 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..579

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

ACG TGC GGA TTC GCC GAC CTC GTG GGG TAC ATC CCG CTC GTA GGC GGC Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly 1 5 10 15	48
CCC GTT GGG GGC GTC GCA AGG GCT CTC GCA CAT GGT GTG AGG GTT CTT Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu 20 25 30	96
GAG GAC GGG GTG AAT TAT GCA ACA GGG AAT CTG CCT GGT TGC TCT TTC Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45	144
TCT ATC TTC ATT CTT GCA CTT CTC TCG TGC CTC ACT GTC CCG GCC TCT Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60	192
GCA GTT CCC TAC CGA AAT GCC TCT GGG ATC TAT CAT GTC ACC AAT GAT Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp 65 70 75 80	240
TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT GAT CTG ATC CTA CAC Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His 85 90 95	288
GCA CCT GGC TGC GTG CCT TGT GTC AGG AAA GAT AAT GTG AGT AGG TGC Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys 100 105 110	336
TGG GTC CAA ATT ACC CCC ACG CTG TCA GCC CCG AGC TTC GGA GCA GTC Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val 115 120 125	384
ACG GCT CCC CTT CGG AGA GCC GTT GAT TAC TTG GTG GGA GGG GCT GCC Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala 130 135 140	432
CTC TGC TCC GCG TTA TAC GTT GGA GAC GCG TGT GGG GCA CTA TTT TTG Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu 145 150 155 160	480
GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAT GCT ACG GTG CAG Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln 165 170 175	528
GAC TGC AAC TGT TCC ATC TAC AGT GGC CAC GTC ACC GGC CAT CAG ATG Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met 180 185 190	576
GCA Ala	579

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

```

Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly
 1           5           10           15
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
          20           25           30
Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
          35           40           45
Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
          50           55           60
Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp
          65           70           75           80
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His
          85           90           95
Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys
          100          105          110
Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val
          115          120          125
Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala
          130          135          140
Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu
          145          150          155          160
Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
          165          170          175
Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met
          180          185          190
Ala

```

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 530 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..530

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 3..527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

CA CCT ACG ACA GCT CTG CTG GTG GCC CAG TTA CTG CGG ATT CCC CAA	47
Pro Thr Thr Ala Leu Val Ala Gln Leu Arg Ile Pro Gln	
1 5 10 15	
GTG GTC ATT GAC ATC ATC GCA GGG AGC CAC TGG GGG GTC TTG TTT GCC	95
Val Val Ile Asp Ile Ile Ala Gly Ser His Trp Gly Val Leu Phe Ala	
20 25 30	
GCC GCA TAC TAT GCA TCG GTG GCT AAC TGG ACC AAG GTC GTG CTG GTC	143
Ala Ala Tyr Tyr Ala Ser Val Ala Asn Trp Thr Lys Val Val Leu Val	
35 40 45	
TTG TTT CTG TTT GCA GGG GTT GAT GCT ACT ACC CAG ATT TCG GGC GGC	191
Leu Phe Leu Phe Ala Gly Val Asp Ala Thr Thr Gln Ile Ser Gly Gly	
50 55 60	
TCC AGC GCC CAA ACG ACG TAT GGC ATC GCC TCA TTT ATC ACC CGC GGC	239
Ser Ser Ala Gln Thr Thr Tyr Gly Ile Ala Ser Phe Ile Thr Arg Gly	
65 70 75	
CGC CAG CAG AAA CTG CAG CTC ATA AAT ACC AAC GGA AGC TGG CAC ATC	287
Ala Gln Gln Lys Leu Gln Leu Ile Asn Thr Asn Gly Ser Trp His Ile	
80 85 90 95	
AAC AGG ACC GCC CTT AAT TGT AAT GAC AGC CTC CAG ACT GGG TTC ATA	335
Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Ile	
100 105 110	
GCC GGC CTC TTC TAC TAC CAT AAG TTC AAC TCT TCT GGA TGC CCG GAT	383
Ala Gly Leu Phe Tyr Tyr His Lys Phe Asn Ser Ser Gly Cys Pro Asp	
115 120 125	
CGG ATG GCT AGC TGT AGG GCC CTT GCC ACT TTT GAC CAG GGC TGG GGA	431
Arg Met Ala Ser Cys Arg Ala Leu Ala Thr Phe Asp Gln Gly Trp Gly	
130 135 140	
ACT ATC AGC TAT GCC AAC ATA TCG GGT CCC AGT GAT GAC AAA CCA TAT	479
Thr Ile Ser Tyr Ala Asn Ile Ser Gly Pro Ser Asp Asp Lys Pro Tyr	
145 150 155	
TGC TGG CAC TAT CCC CCA CGG CCG TGC GGA GTG GTG CCA GCC CAA GAG	527

Cys Trp His Tyr Pro Pro Arg Pro Cys Gly Val Val Pro Ala Gln Glu
 160 165 170 175

GTC
 Val

530

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

Pro Thr Thr Ala Leu Leu Val Ala Gln Leu Leu Arg Ile Pro Gln Val
 1 5 10 15
 Val Ile Asp Ile Ile Ala Gly Ser His Trp Gly Val Leu Phe Ala Ala
 20 25 30
 Ala Tyr Tyr Ala Ser Val Ala Asn Trp Thr Lys Val Val Leu Val Leu
 35 40 45
 Phe Leu Phe Ala Gly Val Asp Ala Thr Thr Gln Ile Ser Gly Gly Ser
 50 55 60
 Ser Ala Gln Thr Thr Tyr Gly Ile Ala Ser Phe Ile Thr Arg Gly Ala
 65 70 75 80
 Gln Gln Lys Leu Gln Leu Ile Asn Thr Asn Gly Ser Trp His Ile Asn
 85 90 95
 Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Ile Ala
 100 105 110
 Gly Leu Phe Tyr Tyr His Lys Phe Asn Ser Ser Gly Cys Pro Asp Arg
 115 120 125
 Met Ala Ser Cys Arg Ala Leu Ala Thr Phe Asp Gln Gly Trp Gly Thr
 130 135 140
 Ile Ser Tyr Ala Asn Ile Ser Gly Pro Ser Asp Asp Lys Pro Tyr Cys
 145 150 155 160
 Trp His Tyr Pro Pro Arg Pro Cys Gly Val Val Pro Ala Gln Glu Val
 165 170 175

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..340

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

C TCG ACC GTT ACC GAA CAT GAC ATA ATG ACC GAA GAG TCC ATT TAC	46
Ser Thr Val Thr Glu His Asp Ile Met Thr Glu Glu Ser Ile Tyr	
1 5 10 15	
CAA TCA TGT GAC TTG CAG CCC GAG GCA CGC GCA GCA ATA CGG TCA CTC	94
Gln Ser Cys Asp Leu Gln Pro Glu Ala Arg Ala Ala Ile Arg Ser Leu	
20 25 30	
ACC CAA CGC CTC TAC TGT GGA GGC CCC ATG TAC AAC AGC AAG GGG CAA	142
Thr Gln Arg Leu Tyr Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln	
35 40 45	
CAG TGT GGT TAT CGC AGA TGC CGC GCC AGC GGC GTT TTC ACC ACC AGT	190
Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser	
50 55 60	
ATG GGC AAC ACC ATG ACG TGC TAC ATC AAG GCT TTA GCC TCC TGT AGA	238
Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ser Cys Arg	
65 70 75	
GCC GCA AGG CTC CGG GAC TGC ACG CTC CTG GTG TGT GGT GAC GAT CTT	286
Ala Ala Arg Leu Arg Asp Cys Thr Leu Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTG GCC ATC TGC GAG ACG CAG GGG ACA CAC GAG GAT GAA GCA AGC CTG	334
Val Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Ser Leu	
100 105 110	
AGA GCC	340
Arg Ala	

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

```

Ser Thr Val Thr Glu His Asp Ile Met Thr Glu Glu Ser Ile Tyr Gln
 1             5             10             15
Ser Cys Asp Leu Gln Pro Glu Ala Arg Ala Ala Ile Arg Ser Leu Thr
                20             25             30
Gln Arg Leu Tyr Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Gln
 35             40             45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met
 50             55             60
Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ser Cys Arg Ala
 65             70             75             80
Ala Arg Leu Arg Asp Cys Thr Leu Leu Val Cys Gly Asp Asp Leu Val
                85             90             95
Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Ser Leu Arg
100             105             110

```

Ala

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

```

C TCA ACC GCC ACC GAA CAT GAC ATA TTG ACT GAA GAG TCC ATA TAC
Ser Thr Ala Thr Glu His Asp Ile Leu Thr Glu Glu Ser Ile Tyr

```

46

Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Asn Leu Arg
 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 163:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 499 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..499

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

ATG AGC ACG AAT CCT AAA CTT CAA AGA AAA ACC AAA CGT AAC ACC AAC	48
Met Ser Thr Asn Pro Lys Leu Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
CGC CGC CCC ATG GAC GTT AAG TTC CCG GGT GGT GGC CAG ATC GTT GGC	96
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly	
20 25 30	
GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG TTG GGT GTG CGC GCG	144
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
ACT CGG AAG ACT TCG GAG CGG TCG CAA CCT CGT GGG AGG CGC CAA CCT	192
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
ATC CCC AAG GCG CGC CGA TCC GAG GGC AGA TCC TGG GCG CAG CCC GGG	240
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly	
65 70 75 80	
TAT CCT TGG CCC CTT TAC GGC AAT GAG GGC TGT GGG TGG GCA GGG TGG	288
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp	
85 90 95	
CTC CTG TCC CCT CGC GGG TCT CGG CCG TCT TGG GGC CCT AAT GAT CCC	336

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro	
100 105 110	
CGG CGG AGG TCC CGC AAC CTG GGT AAG GTC ATC GAT ACC CTA ACA TGC	384
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys	
115 120 125	
GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTA GGC GCC CCC GTG	432
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val	
130 135 140	
GGT GGC GTC GCC AGA GCC CTG GCA CAC GGT GTT AGG GCT GTG GAA GAC	480
Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp	
145 150 155 160	
GGG ATC AAC TAC GCA ACA G	499
Gly Ile Asn Tyr Ala Thr	
165	

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Met Ser Thr Asn Pro Lys Leu Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly	
65 70 75 80	
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp	
85 90 95	
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro	
100 105 110	
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys	
115 120 125	
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val	
130 135 140	

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp
 145 150 155 160

Gly Ile Asn Tyr Ala Thr
 165

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

ATGAGCACGA ATCCTAAACC TCAGAAGAAA ACCAAACGTA ACACCAACCG CCGCCCTATG 60
 GACGTTAAGT TCCAGGCGCG TGGTCAGATC GTTGGCGGAG TTTACTTGTI GCCGCGCAGG 120
 GGCCCCAGST TGGGTGTGCG CGCGACTCGG AAGACTTCGG AGCGGTCGCA ACCTCGTGGG 180
 AGGCGCCAAC CTATCCCCAA GCGCGCCGGA ACCGAGGGCA GATCCTGGGC GCAGCCCCGG 240
 TATCCTTGCG CCCTTTACGG CAATGAGGGC TGTGGGTGGG CAGGGTGGCT CCTGTCCCT 300
 CGCGNTCTC GGNCGTCTTG GGGCCCCAAT GATCCCCGGN GGAGATCCCG CAACTTGGGT 360
 AAGTGCATCG ATACCTTAAC ATGCGGCTTC GCGACCTCA TGGGATACAT CCCGCTTGTA 420
 GCGCCCCCGT TGGGTGGCGT CGCCAGGGCC CTGGCACATG GTGTTAGGGC TGTGGAAGAC 480
 GGGATCAATT ATGCAACAG 499

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn

1	5	10	15
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly			
	20	25	30
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala			
	35	40	45
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro			
	50	55	60
Ile Pro Lys Ala Arg Arg Thr Glu Gly Arg Ser Trp Ala Gln Pro Gly			
	65	70	80
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp			
	85	90	95
Leu Leu Ser Pro Arg Xaa Ser Arg Xaa Ser Trp Gly Pro Asn Asp Pro			
	100	105	110
Arg Xaa Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu			
	115	120	125

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

ACA TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCC GTG GGT GGC GTC GCC AGG GCC CTG GCA CAT GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAA GAC GGG ATC AAT TAT GCA ACA GGG AAC CIT CCC GGT TGC TCC TTT	144

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTC TTG GCG CTC CTC TCG TGC CTG ACT GTT CCC ACA TCG	192
Ser Ile Phe Leu Leu Ala Leu Ser Cys Leu Thr Val Pro Thr Ser	
50 55 60	
GCC GTT AAC TAT CGC AAT GCT TCG GGC ATT TAT CAC ATC ACC AAT GAC	240
Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp	
65 70 75 80	
TGC CCG AAT GCA AGC ATA GTG TAC GAG ACC GAA AAT CAC ATC TTA CAC	288
Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Glu Asn His Ile Leu His	
85 90 95	
CTC CCA GGG TGC GTA CCC TGT GTG AGG ACT GGG AAC CAG TCG CGG TGT	336
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTG GCC CTC ACT CCC ACA GTA GCG TCG CCA TAC GCC GGT GCT CCG	384
Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Ala Gly Ala Pro	
115 120 125	
CTT GAG CCC TTG CGG CGT CAT GTG GAC CTG ATG GTA GGT GCT GCC ACC	432
Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr	
130 135 140	
ATG TGT TCC GCC CTC TAC ATC GGC GAC TTG TGC GGT GGC TTA TTC TTG	480
Met Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu	
145 150 155 160	
GTG GGC CAA ATG TTC ACC TTC CAA CCG CGA CGT CAC TGG ACC ACT CAG	528
Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln	
165 170 175	
GAC TGC AAT TGT TCC ATC TAC ACG GGC CAC ATT ACG GGT CAT CGG ATG	576
Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met	
180 185 190	
GCA	579
Ala	

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

```

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
      20              25              30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
      35              40              45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser
      50              55              60

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp
      65              70              75              80

Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Glu Asn His Ile Leu His
      85              90              95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys
      100             105             110

Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Ala Gly Ala Pro
      115             120             125

Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
      130             135             140

Met Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu
      145             150             155             160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln
      165             170             175

Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met
      180             185             190

Ala

```

(2) INFORMATION FOR SEQ ID NO: 169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..579
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

ACA TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCC GTG GGT GGC GTC GCC AGA GCC CTG GCA CAC GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAA GAC GGG ATC AAC TAC GCA ACA GGG AAT CTC CCC GGT TGC TCC TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTC TTG GCA CTT CTC TCG TGC CTC ACT GTT CCC GCG TCG	192
Ser Ile Phe Leu Leu Ala Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GGC GTT AAC TAT CGC AAT GCT TCG GGC GTT TAT CAC ATC ACC AAC GAC	240
Gly Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp	
65 70 75 80	
TGC CCG AAT GCG AGC ATA GTG TAC GAG ACC GAC AAT CAC ATC TTA CAC	288
Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Asp Asn His Ile Leu His	
85 90 95	
CTC CCA GGG TGC GTA CCC TGT GTG AAG ACC GGG AAC CAG TCG CGG TGT	336
Leu Pro Gly Cys Val Pro Cys Val Lys Thr Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTG GCC CTC ACT CCC ACA GTG GCG TCG CCT TAC GTC GGT GCT CCG	384
Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Val Gly Ala Pro	
115 120 125	
CTC GAG CCC TTG CCG CGC CAT GTG GAC CTG ATG GTA GGT GCT GCC ACC	432
Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr	
130 135 140	
GTG TGC TCC GCC CTC TAC GTC GGC GAC CTG TGC GGT GGC TTA TTC TTG	480
Val Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Leu Phe Leu	
145 150 155 160	
GTA GGC CAA ATG TTC ACC TTC CAA CCG CGA CGC CAC TGG ACG ACC CAG	528
Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln	
165 170 175	
GAC TGT AAT TGT TCC ATC TAC GCA GGC CAT ATT ACG GGC CAT CGG ATG	576
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Arg Met	
180 185 190	
GCT	579
Ala	

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

```

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1             5             10             15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
                20             25             30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
        35             40             45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
        50             55             60

Gly Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp
        65             70             75             80

Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Asp Asn His Ile Leu His
        85             90             95

Leu Pro Gly Cys Val Pro Cys Val Lys Thr Gly Asn Gln Ser Arg Cys
        100            105            110

Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Val Gly Ala Pro
        115            120            125

Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
        130            135            140

Val Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Leu Phe Leu
        145            150            155            160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln
        165            170            175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Arg Met
        180            185            190

Ala

```

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..579

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

ACA TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTG GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCT GTT GGT GGC GTC GCC AGA GCC CTT GCG CAC GGC GTC AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAA GAC GGG ATT AAC TAT GCA ACA GGG AAC CTT CCT GGT TGC TCC TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTT CTG GCA CTT CTC TCG TGC CTG ACT GTC CCC GCC TCG	192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCT GTG CAT TAT CAC AAC ACC TCG GGC ATC TAC CAC CTC ACC AAT GAC	240
Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Leu Thr Asn Asp	
65 70 75 80	
TGC CCT AAC TCT AGC ATA GTC TTT GAG GCA GTC CAT CAC ATC TTG CAC	288
Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Val His His Ile Leu His	
85 90 95	
CTT CCA GGA TGC GTC CCT TGT GTA AGA ACT GGG AAC CAG TCT CGG TGC	336
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTA GCC TTG ACC CCC ACG CTG GCC GCG CCA TAC CTT GGC GCT CCA	384
Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Pro Tyr Leu Gly Ala Pro	
115 120 125	
CTC GAG TCC ATG CCG CGT CAC GTG GAT TTG ATG GTG GGC ACT GCT ACA	432
Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr	
130 135 140	
TTG TGC TCA GCA CTC TAC GTT GGG GAC CTG TGC GGG GGC ATA TTC CTA	480
Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Ile Phe Leu	
145 150 155 160	
GCG GGC CAG ATG TTC ACC TTC CGG CCC CGC CTC CAT TGG ACC ACC CAG	528
Ala Gly Gln Met Phe Thr Phe Arg Pro Arg Leu His Trp Thr Thr Gln	
165 170 175	

GAG TGC AAT TGT TCC ACC TAT CCG GGC CAC ATC ACG GGT CAT AGA ATG 576
 Glu Cys Asn Cys Ser Thr Tyr Pro Gly His Ile Thr Gly His Arg Met
 180 185 190

CGC 579
 Ala

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
 50 55 60

Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Leu Thr Asn Asp
 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Val His His Ile Leu His
 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys
 100 105 110

Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Pro Tyr Leu Gly Ala Pro
 115 120 125

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr
 130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Ile Phe Leu
 145 150 155 160

Ala Gly Gln Met Phe Thr Phe Arg Pro Arg Leu His Trp Thr Thr Gln
 165 170 175

Glu Cys Asn Cys Ser Thr Tyr Pro Gly His Ile Thr Gly His Arg Met
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 173:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 579 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

ACG TGC GGT TCC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Ser Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCT GTG GGT GGC GTC GCC AGG GCC TTG GCG CAT GGC GTC AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGG ATA AAC TAT GCA ACA GGG AAC CTT CCT GGT TGC TCT TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTT CTG GCA CTT CTC TCG TGC CTG ACT GTC CCC GCC TCA	192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCT GTG CAT TAT CAC AAC ACC TCG GGC ATC TAT CAC ATC ACT AAT GAC	240
Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Ile Thr Asn Asp	
65 70 75 80	
TGC CCT AAC TCT AGC ATA GTC TTT GAG GCA GAG CAT CAC ATC TTG CAT	288
Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Glu His His Ile Leu His	
85 90 95	
CTT CCA GGA TGC GTC CCC TGT GTG AGA ACT GGG AAC CAG TCA CGA TGC	336
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG ATA GCC TTG ACC CCT ACG TTG GCC GCG CCA CAC ATT GGC GCT CCA	384
Trp Ile Ala Leu Thr Pro Thr Leu Ala Ala Pro His Ile Gly Ala Pro	

115	120	125	
CTT GAG TCC ATG CGA CGT CAT GTG GAT TTG ATG GTA GGC ACT GCC ACA			432
Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr			
130	135	140	
TTG TGC TCC GCA CTC TAC ATT GGA GAT CTG TGC GGA GGC ATA TTT CTA			480
Leu Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Ile Phe Leu			
145	150	155	160
GTG GGC CAG ATG TTC AAC TTC AGG CCC CGC CTG CAC TGG ACC ACC CAG			528
Val Gly Gln Met Phe Asn Phe Arg Pro Arg Leu His Trp Thr Thr Gln			
165	170	175	
GAG TGC AAT TGT TCC ATC TAT CCA GGC CAC ATC ACG GGT CAC AGA ATG			576
Glu Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met			
180	185	190	
GCG			579
Ala			

(2) INFORMATION FOR SEQ ID NO: 174:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

Thr	Cys	Gly	Ser	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala
1				5					10					15	
Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Ala	Val
	20				25								30		
Glu	Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe
	35				40							45			
Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser
	50				55						60				
Ala	Val	His	Tyr	His	Asn	Thr	Ser	Gly	Ile	Tyr	His	Ile	Thr	Asn	Asp
	65				70				75					80	
Cys	Pro	Asn	Ser	Ser	Ile	Val	Phe	Glu	Ala	Glu	His	His	Ile	Leu	His
			85					90					95		
Leu	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Thr	Gly	Asn	Gln	Ser	Arg	Cys
		100						105					110		
Trp	Ile	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Pro	His	Ile	Gly	Ala	Pro
	115						120						125		

224

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr
 130 135 140
 Leu Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Ile Phe Leu
 145 150 155 160
 Val Gly Gln Met Phe Asn Phe Arg Pro Arg Leu His Trp Thr Thr Gln
 165 170 175
 Glu Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met
 180 185 190
 Ala

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

ACG TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCT GTG GGT GGC GTC GCC AGG GCC TTG GCA CAT GGT GTC AGG GCC GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGG ATT AAC TAT GCA ACA GGG AAT CTT CCC GGT TGC TCC TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTT CTA GCA CTT CTC TCG TGC TTG ACT GTC CCG GCC TCG	192
Ser Ile Phe Leu Leu Ala Leu Leu-Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCG CAG CAC TAC CGG AAC ATC TCG GGC ATT TAT CAC GTC ACC AAT GAC	240
Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp	

225

65	70	75	80
TGC CCG AAC TCT AGT ATA GTG TAT GAA GCT GAC CAT CAT ATC ATG CAT Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His	85	90	95
CTA CCA GGG TGT GTG CCT TGC GTG AGA ACC GGG AAC ACC TCG CGC TGC Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys	100	105	110
TGG GTT CCT TTA ACA CCC ACT GTG GCT GCC CCC TAT GTT GGC GCG CCG Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro	115	120	125
CTC GAA TCC ATG CGG CGG CAC GTG GAC TTA ATG GTG GGT GCC GCC ACC Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr	130	135	140
GTC TGC TCG GCC CTG TAC ATC GGA GAC CTT TGC GGA GGT GTC TTC CTG Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu	145	150	155
GTC GGG CAG ATG TTC ACC TTC CGG CCG CGC CAT TGG ACT ACC CAG Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln	165	170	175
GAC TGC AAC TGC TCT ATC TAT GAT GGC CAC ATC ACC GGC CAT AGA ATG Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg Met	180	185	190
GCT Ala			

288

336

384

432

480

528

576

579

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
 50 55 60

Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp
 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His
 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys
 100 105 110

Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro
 115 120 125

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
 130 135 140

Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu
 145 150 155 160

Val Gly Gln Met Phe Thr Phe Arg Pro Arg His Trp Thr Thr Gln
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg Met
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

ACG TGC GGG TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCT 48
 Thr Cys Gly Phe Ala Asp Leu Met-Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

CCA GTA GGA GGC GTC GCC AGA GCC TTG GCG CAT GGC GTC AGG GCT GTG 96
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val

20	25	30	
GAG GAC GGG ATC AAT TAC GCA ACA GGG AAC CTT CCC GGC TGC TCC TTT Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45			144
TCT ATC TTC CTC TTG GTA CTT CTC TCG CGC CTA ACT GTC CCA GCG TCT Ser Ile Phe Leu Leu Val Leu Leu Ser Arg Leu Thr Val Pro Ala Ser 50 55 60			192
GCT CAG CAC TAC CGG AAT GCA TCG GGC ATC TAC CAT GTC ACC AAC GAC Ala Gln His Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp 65 70 75 80			240
TGC CCG AAC TCC AGT ATT GTG TAT GAA GCC GAC CAT CAC ATC ATG CAC Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His 85 90 95			288
CTA CCC GGG TGT GTG CCC TGT GTA AGA ACT GGG AAT GTC TCG CGT TGC Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Val Ser Arg Cys 100 105 110			336
TGG ATT CCT TTA ACA CCC ACT GTA GCC GTC CCC TAC CTC GGG GCT CCA Trp Ile Pro Leu Thr Pro Thr Val Ala Val Pro Tyr Leu Gly Ala Pro 115 120 125			384
CTT ACG TCT GTA CGG CAG CAT GTG GAC CTG ATG GTG GGG GCG GCC ACC Leu Thr Ser Val Arg Gln His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140			432
TTA TGC TCT GCC CTC TAC ATC GGA GAC CAT TGC GGA GGT GTC TTC TTG Leu Cys Ser Ala Leu Tyr Ile Gly Asp His Cys Gly Gly Val Phe Leu 145 150 155 160			480
GCA GGG CAG ATG GTC AGT TTC CAA CCC CGG CGT CAT TGG ACT ACC CAG Ala Gly Gln Met Val Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165 170 175			528
GAT TGC AAC TGT TCC ATC TAT GTG GGC CAC ATC ACC GGC CAC AGG ATG Asp Cys Asn Cys Ser Ile Tyr Val Gly His Ile Thr Gly His Arg Met 180 185 190			576
GCC Ala			579

(2) INFORMATION FOR SEQ ID NO: 178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

```

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
  1             5             10             15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
          20             25             30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
          35             40             45

Ser Ile Phe Leu Leu Val Leu Leu Ser Arg Leu Thr Val Pro Ala Ser
          50             55             60

Ala Gln His Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp
          65             70             75             80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His
          85             90             95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Val Ser Arg Cys
          100            105            110

Trp Ile Pro Leu Thr Pro Thr Val Ala Val Pro Tyr Leu Gly Ala Pro
          115            120            125

Leu Thr Ser Val Arg Gln His Val Asp Leu Met Val Gly Ala Ala Thr
          130            135            140

Leu Cys Ser Ala Leu Tyr Ile Gly Asp His Cys Gly Gly Val Phe Leu
          145            150            155            160

Ala Gly Gln Met Val Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln
          165            170            175

Asp Cys Asn Cys Ser Ile Tyr Val Gly His Ile Thr Gly His Arg Met
          180            185            190

Ala

```

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

AQCTGCGGGT	TGCGCGACCT	CATGGGATAC	ATCCCGCTCG	TAGGCGCCCC	CGTGGGAGGC	60
GTCGCCAGAR	CTCTGGCGCA	TGGCGTCAGG	GCTCTGGAAG	ACGGGATCAA	TTATGCAACA	120
GGGAATCTTC	CTGGTTGCTC	TTTCTCTATC	TCCCTTCTTG	AACCTTCTTC	GTGCGTGAAT	180
GTTCGCCCTC	CAGCCATCCA	CTATCGCAAT	GCTTCGGACG	GTATTATAT	CACCAATGAT	240
TGCCGGAAT	CTAGCATAGT	GTATGAAGCC	GAGAACCACA	TCTTGACCT	TCCGGGGTGT	300
ATACCTCTGT	TGAAGACCG	GAATCACTCG	CGGTGCTGGG	TGGCTCTCAC	CCCCACGCTG	360
GCGGCCCCAC	ACCTACGTGC	TCCGCTTTTG	TCCTTACGGG	CGCATGTGGA	CCTAATGGTG	420
GGGGCCGCCA	CGGCATGCTC	CGCTTTTAC	ATTGGAGATC	TGTGCGGGG	TGTGTTTTTG	480
GCGGCCCAAC	TGTTCACTAT	CCGCCACGC	ATTCAATGAAA	CACTCAGGA	CTGCAATTGC	540
TCCATCTACT	CAGGGCACAT	CACGGGTNNN	NNNNNNNNN			579

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Gly	Ala	1	5	10	15	
Pro	Val	Gly	Gly	Val	Ala	Arg	Xaa	Leu	Ala	His	Gly	Val	Arg	Ala	Leu	20	25	30	
Glu	Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	35	40	45	
Ser	Ile	Ser	Leu	Leu	Glu	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	50	55	60	
Ala	Ile	His	Tyr	Arg	Asn	Ala	Ser	Asp	Gly	Tyr	Tyr	Ile	Thr	Asn	Asp	65	70	75	80
Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Glu	Asn	His	Ile	Leu	His	85	90	95	
Leu	Pro	Gly	Cys	Ile	Pro	Cys	Val	Lys	Thr	Gly	Asn	Gln	Ser	Arg	Cys	100	105	110	

Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Pro His Leu Arg Ala Pro
 115 120 125
 Leu Ser Ser Leu Arg Ala His Val Asp Leu Met Val Gly Ala Ala Thr
 130 135 140
 Ala Cys Ser Ala Phe Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu
 145 150 155 160
 Ala Gly Gln Leu Phe Thr Ile Arg Pro Arg Ile His Glu Thr Thr Gln
 165 170 175
 Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Ile Thr Gly Xaa Xaa Xaa
 180 185 190
 Xaa

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

GCSTGCGGCT TCGCCGATCT CATGGGATAC ATCCGCTCG TAGGCSCCCC CGTGGGTGGC	60
GTCCCGCAGAG CCTTGGCGCA CGTGTTAGG GCTGTGGAGG ACGGGATTAA CTACGCAACA	120
GGGAATCTTC CTGGTTGCTC TTCTCTATC TNCCTTCTGG CACTTCTCTC GTGCCTGACT	180
GTCCCGGCCT CGGCTCAGCA CTACCGGAAT GTCTCGGGCA TCTACCAAGT CACCAATGAT	240
TGCCCGAATT CCAGCATAGT GTATGAAGCC GATCACCACA TCATGCACCT ACCAGGGTGC	300
ATACCTCTGC TGAGGACCGG GAACGTTTCG CGTGCTGGG TATCTCTGAC ACCTACTGTG	360
GCTGCTCCCT ACCTCGGGGC TCCGCTTACG TCGCTACGGC GGCATGTGGA TTTGATGGTG	420
GGTGCAGCCA CCTTTGCTC TGCCCTCTAC GTCGGAGACC TCTGTGGAGG TGTCTTCTTA	480

GTGGGACAGA TGTTACACCTT CCAGCCGCGC CGCCACTGGA CCACTCAGGA CTGCAACTGC 540
 TCCATTACG TCGGCCACAT CACAGGCCAC AGAATGGCT 579

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Ala	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	1	5	10	15
Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Ala	Val	20	25	30	
Glu	Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	35	40	45	
Ser	Ile	Xaa	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	50	55	60	
Ala	Gln	His	Tyr	Arg	Asn	Val	Ser	Gly	Ile	Tyr	His	Val	Thr	Asn	Asp	65	70	75	80
Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	His	His	Ile	Met	His	85	90	95	
Leu	Pro	Gly	Cys	Ile	Pro	Cys	Val	Arg	Thr	Gly	Asn	Val	Ser	Arg	Cys	100	105	110	
Trp	Val	Ser	Leu	Thr	Pro	Thr	Val	Ala	Ala	Pro	Tyr	Leu	Gly	Ala	Pro	115	120	125	
Leu	Thr	Ser	Leu	Arg	Arg	His	Val	Asp	Leu	Met	Val	Gly	Ala	Ala	Thr	130	135	140	
Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys	Gly	Gly	Val	Phe	Leu	145	150	155	160
Val	Gly	Gln	Met	Phe	Thr	Phe	Gln	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln	165	170	175	
Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Val	Gly	His	Ile	Thr	Gly	His	Arg	Met	180	185	190	
Ala																			

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

ACC TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCT GTG GGT GGC GTC GCC AGG GCC CTA GAA CAC GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGT ATT AAT TAT GCA ACA GGG AAT CTC CCC GGT TGC TCT TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TCC CTC TTG GCA CTT CTT TCG TGC CTG ACT GTT CCC ACC TCA	192
Ser Ile Ser Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	
50 55 60	
GCC GTC AAC TAT CGC AAC GCC TCG GGC GTC TAT CAT ATC ACC AAT GAC	240
Ala Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp	
65 70 75 80	
TGC CCG AAT TCG AGC ATA GTG TAC GAG GCT GAC TAC CAC ATC CTA CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Tyr His Ile Leu His	
85 90 95	
CTC CCT GGG TGC TTA CCC TGC GTG AGG GTT GGG AAT CAG TCA CGC TGC	336
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTG GCC CTT ACT CCC ACC GTG GCG GCG CCT TAC GTT GGT GCT CCG	384
Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro	

115	120	125	
CTA GAA TCC CTC CGG AGT CAT GTG GAT CTG ATG GTA GGT GCT GCT ACT			432
Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr			
130	135	140	
GTG TGC TCC GCT CTT TAC ATC GGG GAC CTG TGC GGT GGC GTA TTT TTG			480
Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu			
145	150	155	160
GTT GGT CAG ATG TTT TCT TTC CAG CCG CGA CGC CAC TGG ACC ACG CAG			528
Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln			
165	170	175	
GAC TGC AAT TGT TCT ATC TAC GCG GGG CAC GTT ACG GGC CAC AGG ATG			576
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg Met			
180	185	190	
GCA			579
Ala			

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala			
1	5	10	15
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val			
20	25	30	
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe			
35	40	45	
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser			
50	55	60	
Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp			
65	70	75	80
Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Glu Asn His Ile Leu His			
85	90	95	
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys			
100	105	110	
Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Ala Gly Ala Pro			
115	120	125	
Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr			
130	135	140	

Met Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu
 145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 182:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Ala Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45

Ser Ile Ser Phe Trp His Phe Ser Arg Ala * Leu Ser Arg Pro Arg
 50 55 60

Leu Ser Thr Thr Gly Met Ser Arg Ala Ser Thr Thr Ser Pro Met Ile
 65 70 75 80

Ala Arg Ile Pro Ala * Cys Met Lys Pro Ile Thr Thr Ser Cys Thr
 85 90 95

Tyr Gln Gly Ala Tyr Pro Ala * Gly Pro Gly Thr Phe Arg Ala Ala
 100 105 110

Gly Tyr Leu * His Leu Leu Trp Leu Leu Pro Thr Ser Gly Leu Arg
 115 120 125

Leu Arg Arg Tyr Gly Gly Met Trp Ile * Trp Trp Val Gln Pro Pro
 130 135 140

Phe Ala Leu Pro Ser Thr Ser Glu Thr Ser Val Glu Val Ser Ser *
 145 150 155 160

Trp Asp Arg Cys Ser Pro Ser Ser Arg Ala Ala Thr Gly Pro Leu Arg
 165 170 175

Thr Ala Thr Ala Pro Phe Thr Ser Ala Thr Ser Gln Ala Thr Glu Trp

180

185

190

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCC GTG GGT GGC GTC GCC AGA GCC CTG GAA CAT GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGC ATC AAT TAT GCA ACA GGG AAT CTC CCC GGT TGC TCT TTC	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TAC CTC TTG GCA CTT CTC TCG TGC CTG ACT GTT CCC ACC TCG	192
Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	
50 55 60	
GCC ATC CAC TAT CGC AAT GCC TCG GGC GTC TAC CAC GTC ACC AAT GAC	240
Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp	
65 70 75 80	
TGC CCG AAC TCG AGC ATA GTG TAC GAG GCC GAC CAC CAC ATC CTA CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His	
85 90 95	
CTT CCA GGG TGC TTA CCC TGT GTG AGG GTT GGG AAT CAG TCA CGT TGT	336
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTG GCC CTC TCT CCC ACC GTG GCG GCG CCT TAC ATC GGT GCT CCA	384

Trp	Val	Ala	Leu	Ser	Pro	Thr	Val	Ala	Ala	Pro	Tyr	Ile	Gly	Ala	Pro		
	115						120					125					
GTT	GAA	TCC	TTC	CGG	AGA	CAC	GTG	GAC	ATG	ATG	GTG	GGC	GCT	GCT	ACT	432	
Val	Glu	Ser	Phe	Arg	Arg	His	Val	Asp	Met	Met	Val	Gly	Ala	Ala	Thr		
	130					135					140						
GTG	TGC	TCC	GCT	CTC	TAT	ATT	GGG	GAC	TTG	TGT	GGT	GGC	GTA	TTC	TTG	480	
Val	Cys	Ser	Ala	Leu	Tyr	Ile	Gly	Asp	Leu	Cys	Gly	Gly	Val	Phe	Leu		
	145					150				155				160			
GTT	GGT	CAG	ATG	TTT	TCT	TTC	CGG	CCA	CGA	CGC	CAC	TGG	ACT	ACG	CAG	528	
Val	Gly	Gln	Met	Phe	Ser	Phe	Arg	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln		
			165						170					175			
GAC	TGC	AAT	TGT	TCC	ATC	TAC	GCG	GGG	CAC	ATC	ACT	GGC	CAC	GGA	ATG	576	
Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Ala	Gly	His	Ile	Thr	Gly	His	Gly	Met		
			180					185						190			
GCA																579	
Ala																	

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala		
1				5					10					15			
Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Glu	His	Gly	Val	Arg	Ala	Val		
				20				25					30				
Glu	Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe		
		35					40					45					
Ser	Ile	Tyr	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Thr	Ser		
	50				55					60							
Ala	Ile	His	Tyr	Arg	Asn	Ala	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp		
	65				70				75					80			
Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	His	His	Ile	Leu	His		
				85					90					95			
Leu	Pro	Gly	Cys	Leu	Pro	Cys	Val	Arg	Val	Gly	Asn	Gln	Ser	Arg	Cys		
			100					105					110				
Trp	Val	Ala	Leu	Ser	Pro	Thr	Val	Ala	Ala	Pro	Tyr	Ile	Gly	Ala	Pro		
	115						120						125				

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Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr
    130                      135                      140

Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu
    145                      150                      155                      160

Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln
                      165                      170                      175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met
    180                      185                      190

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Ala

(2) INFORMATION FOR SEQ ID NO: 187:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 579 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..579

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

```

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC      48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
    1                      5                      10                      15

CCT GTG GGT GGC GTC GCC AGG GCC CTG GCA CAC GGT GTT AGG GCT GTG      96
Pro Val Gly Ile Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
                      20                      25                      30

GAG GAC GGG ATC AAT TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC      144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
                      35                      40                      45

TCT ATC TTC CTC TTG GCA CTT CTT-TCG TGC CTG ACT GTT CCC ACC TCG      192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser
    50                      55                      60

GCC GTC AAC TAT CGC AAT GCC TCG GGC ATC TAT CAC ATC ACC AAT GAC      240

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Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp	
65 70 75 80	
TGC CCG AAC TCG AGC ATA GTG TAC GAG ACC GAG CAC CAC ATC CTA CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Ile Leu His	
85 90 95	
CTC CCA GGG TGT TTA CCC TGC GTG AGG GTT GGG AAT CAG TCA CGC TGC	336
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTG GCC CTC ACT CCC ACC GTG GCG GCG CCT TAC ATC GGC GCT CCG	384
Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro	
115 120 125	
CTT GAA TCC CTC CGG AGT CAT GTG GAT CTG ATG GTA GGT GCC GCT ACT	432
Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr	
130 135 140	
GCG TGC TCC GCT CTT TAC ATC GGA GAC CTG TGC GGT GGC GTA TTT TTG	480
Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu	
145 150 155 160	
GTT GGT CAG ATG TTC TCT TTC CAG CCG CGG CGC CAC TGG ACT ACG CAG	528
Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln	
165 170 175	
GAC TGC AAT TGT TCC ATC TAC GCG GCG CAC GTT ACG GGC CAC AGG ATG	576
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg Met	
180 185 190	
GCA	579
Ala	

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	
50 55 60	

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp
 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Ile Leu His
 85 90 95

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys
 100 105 110

Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro
 115 120 125

Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr
 130 135 140

Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu
 145 150 155 160

Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg Met
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

ACG TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

48

CCC GTT GGG GGC GTC GCC AGG GCC CTG GCG CAT GGC GTC AGG GCT GTG Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20 25 30	96
GAG GAC GGG ATT AAC TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45	144
TCT ATC TTC CTC CTG GCA CTT CTT TCG TGC CTC ACT GTC CCA GCG TCA Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60	192
GCT GAG CAC TAC CGG AAT GCT TCG GGC ATC TAT CAC ATC ACC AAT GAC Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp 65 70 75 80	240
TGT CCG AAT TCC AGC GTA GTC TAT GAA ACT GAC CAC CAT ATA TTG CAC Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His 85 90 95	288
TTG CCG GGG TGC GTA CCC TGC GTG AGG GCC GGG AAC GTG TCT CGT TGC Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys 100 105 110	336
TGG ACG CCG GTA ACA CCT ACG GTG GCT GCC GTA TCC ATG GAC GCT CCG Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro 115 120 125	384
CTC GAG TCC TTC CGG CGG CAT GTG GAC CTA ATG GTA GGT GCG GCC ACC Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140	432
GTG TGT TCT GTC CTC TAT GTT GGA GAC CTC TGT GGA GGT GCT TTC CTA Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu 145 150 155 160	480
GTG GGG CAG ATG TTC ACC TTC CAG CCG CGT CGC CAC TGG ACC ACG CAG Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165 170 175	528
GAT TGT AAT TGC TCC ATC TAT ACT GGC CAT ATC ACC GGC CAC AGG ATG Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met 180 185 190	576
GCG Ala	579

(2) INFORMATION FOR SEQ ID NO: 190:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS

(B) LOCATION: 1..289

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC	48
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
CGC CGC CCC ATG GAC GTT AAG TTC CCG GGC GGT GGC CAG ATC GTT GGT	96
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
GGA GTT TAC TTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG	144
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
ACT AGG AAG ACT TCG GAG CGG TCG CAA CCT CGT GGG AGA CGT CAG CCT	192
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
ATC CCC AAG GCA CGT CGA TCT GAG GGA AGG TCC TGG GCT CAG CCC GGG	240
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly	
65 70 75 80	
TAC CCA TGG CCT CTT TAC GGT AAT GAG GGT TGT GGG TGG GCA GGA TGG G	289
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp	
85 90 95	

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly	

Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro		
			100					105					110				
CGG	CGG	AGA	TCG	CGC	AAT	CTG	GGT	AAG	GTC	ATC	GAT	ACC	CTG	ACG	TGC		384
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys		
			115				120						125				
GGC	TTC	GCC	GAC	CTC	ATG	GGA	TAC	ATC	CCG	CTC	GTG	GGC	GCC	CCC	GTC		432
Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Val		
			130				135					140					
GGG	GGC	GTC	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	AGG	GCT	GTG	GAG	GAC		480
Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Ala	Val	Glu	Asp		
			145		150				155					160			
GGG	ATT	AAC	TAT	CGA	CAG												498
Gly	Ile	Asn	Tyr	Arg	Gln												
					165												

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn		
1					5					10					15		
Arg	Arg	Pro	Met	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly		
			20					25					30				
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala		
			35				40					45					
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro		
			50			55					60						
Ile	Pro	Lys	Ala	Arg	Arg	Ser	Glu	Gly	Arg	Ser	Trp	Ala	Gln	Ala	Gly		
			65		70				75						80		
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp		
			85				90					95					
Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro		
			100				105					110					
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys		
			115				120					125					
Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Val		
			130			135					140						

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp
 145 150 155 160

Gly Ile Asn Tyr Arg Gln
 165

(2) INFORMATION FOR SEQ ID NO: 195:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 579 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

ACG TGC GGA TTC GCC GAC CTC GTG GGG TAC ATC CCG CTC GTA GGC GGC	48
Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly	
1 5 10 15	
CCC GTT GGG GGC GTC GCA AGG GCT CTC GCA CAT GGT GTG AGG GTT CTT	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu	
20 25 30	
GAG GAC GGG GTG AAT TAT GCA ACA GGG AAT CTG CCT GGT TGC TCT TTC	144
Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC ATT CTT GCA CTT CTC TCG TGC CTC ACT GTC CCG GCC TCT	192
Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCA GTT CCC TAC CGA AAT GCC TCT GGG ATC TAT CAT GTC ACC AAT GAT	240
Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp	
65 70 75 80	
TGC CCA AAC TCT TCC ATA GTC TAT-GAG GCA GAT GAT CTG ATC CTA CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His	
85 90 95	
GCA CCT GGC TGC GTG CCT TGT GTC AGS AAA GAT AAT GTG AGT AGG TGC	336

Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Lys	Asp	Asn	Val	Ser	Arg	Cys	
		100						105					110			
TGG	GTC	CAA	ATT	ACC	CCC	ACG	CTG	TCA	GCC	CCG	AGC	TTC	GGA	GCA	GTC	384
Trp	Val	Gln	Ile	Thr	Pro	Thr	Leu	Ser	Ala	Pro	Ser	Phe	Gly	Ala	Val	
		115					120					125				
ACG	GCT	CCC	CTT	CGG	AGA	GCC	GTT	GAT	TAC	TTG	GTG	GGA	GGG	GCT	GCC	432
Thr	Ala	Pro	Leu	Arg	Arg	Ala	Val	Asp	Tyr	Leu	Val	Gly	Gly	Ala	Ala	
		130				135				140						
CTC	TGC	TCC	GCG	TTA	TAC	GTT	GGA	GAC	GCG	TGT	GGG	GCA	CTA	TTT	TTG	480
Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Ala	Cys	Gly	Ala	Leu	Phe	Leu	
145				150					155					160		
GTA	GGC	CAA	ATG	TTC	ACC	TAT	AGG	CCT	CGC	CAG	CAT	GCT	ACG	GTG	CAG	528
Val	Gly	Gln	Met	Phe	Thr	Tyr	Arg	Pro	Arg	Gln	His	Ala	Thr	Val	Gln	
		165						170				175				
GAC	TGC	AAC	TGT	TCC	ATC	TAC	AGT	GGC	CAC	GTG	ACC	GGC	CAT	CAG	ATG	576
Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Ser	Gly	His	Val	Thr	Gly	His	Gln	Met	
		180					185					190				
GCA																579
Ala																

(2) INFORMATION FOR SEQ ID NO: 196:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Thr	Cys	Gly	Phe	Ala	Asp	Leu	Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Gly	
1				5				10					15			
Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	
		20					25					30				
Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	
		35				40					45					
Ser	Ile	Phe	Ile	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	
		50				55				60						
Ala	Val	Pro	Tyr	Arg	Asn	Ala	Ser	Gly	Ile	Tyr	His	Val	Thr	Asn	Asp	
	65				70				75					80		
Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asp	Leu	Ile	Leu	His	
			85					90					95			
Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Lys	Asp	Asn	Val	Ser	Arg	Cys	
		100						105					110			

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val
 115 120 125

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala
 130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu
 145 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 579 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCC GTG GGT GGC GTC GCC AGA GCC CTG GAA CAT GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGC ATC AAT TAT GCA ACA GGG AAT CTC CCC GGT TGC TCT TTC	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TAC CTC TTG GCA CTT CTC TCG TGC CTG ACT GTT CCC ACC TCG	192

Ser	Ile	Tyr	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Thr	Ser	
50						55					60					
GCC	ATC	CAC	TAT	CGC	AAT	GCC	TCG	GGC	GTC	TAC	CAC	GTC	ACC	AAT	GAC	240
Ala	Ile	His	Tyr	Arg	Asn	Ala	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp	
65				70				75						80		
TGC	CCG	AAC	TCG	AGC	ATA	GTG	TAC	GAG	GCC	GAC	CAC	CAC	ATC	CTA	CAC	288
Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	His	His	Ile	Leu	His	
				85				90						95		
CTT	CCA	GGG	TGC	TTA	CCC	TGT	GTG	AGG	GTT	GGG	AAT	CAG	TCA	CGT	TGT	336
Leu	Pro	Gly	Cys	Leu	Pro	Cys	Val	Arg	Val	Gly	Asn	Gln	Ser	Arg	Cys	
			100					105					110			
TGG	GTG	GCC	CTC	TCT	CCC	ACC	GTG	GCG	GCG	CCT	TAC	ATC	GGT	GCT	CCA	384
Trp	Val	Ala	Leu	Ser	Pro	Thr	Val	Ala	Ala	Pro	Tyr	Ile	Gly	Ala	Pro	
			115				120						125			
GTT	GAA	TCC	TTC	CGG	AGA	CAC	GTG	GAC	ATG	ATG	GTG	GGC	GCT	GCT	ACT	432
Val	Glu	Ser	Phe	Arg	Arg	His	Val	Asp	Met	Met	Val	Gly	Ala	Ala	Thr	
	130					135					140					
GTG	TGC	TCC	GCT	CTC	TAT	ATT	GGG	GAC	TTG	TGT	GGT	GGC	GTA	TTC	TTG	480
Val	Cys	Ser	Ala	Leu	Tyr	Ile	Gly	Asp	Leu	Cys	Gly	Gly	Val	Phe	Leu	
145				150					155					160		
GTT	GGT	CAG	ATG	TTT	TCT	TTC	CGG	CCA	CGA	CGC	CAC	TGG	ACT	ACG	CAG	528
Val	Gly	Gln	Met	Phe	Ser	Phe	Arg	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln	
			165					170						175		
GAC	TGC	AAT	TGT	TCC	ATC	TAC	GCG	GGG	CAC	ATC	ACT	GGC	CAC	GGA	ATG	576
Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Ala	Gly	His	Ile	Thr	Gly	His	Gly	Met	
			180					185						190		
GCA																579
Ala																

(2) INFORMATION FOR SEQ ID NO: 198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	
1				5					10					15		
Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Glu	His	Gly	Val	Arg	Ala	Val	
			20					25					30			
Glu	Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	

35	40	45
Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser		
50	55	60
Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp		
65	70	75
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His		
85	90	95
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys		
100	105	110
Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro		
115	120	125
Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr		
130	135	140
Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu		
145	150	155
Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln		
165	170	175
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met		
180	185	190
Ala		

(2) INFORMATION FOR SEQ ID NO: 199:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1470 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..1470

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 2..1467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

A TCA CCA CCG GAG CTT CTA TCA CAT ACT CCA CTT ACG GCA AGT TCC Ser Pro Pro Glu Leu Ser His Thr Pro Leu Thr Ala Ser Ser 1 5 10 15	46
TTG CTG ATG GAG GGT GTT CAG GCG GCG CGC ATG ACG TGA TCA TAT GCG Leu Leu Met Glu Gly Val Gln Ala Ala Arg Met Thr * Ser Tyr Ala 20 25 30	94
ACG AGT GCC ATT CCC AGG ACG CCA CCA CCA TTC TTG GGA TAG GCA CTG Thr Ser Ala Ile Pro Arg Thr Pro Pro Pro Phe Leu Gly * Ala Leu 35 40 45	142
TCC TTG ACC AGG CAG AGA CGG CTG GAG CTA GGC TCG TCG TCT TGG CCA Ser Leu Thr Arg Gln Arg Arg Leu Glu Leu Gly Ser Ser Ser Trp Pro 50 55 60	190
CGG CCA CCC CTC CCG GCA GTG TGA CAA CGC CCC ACC CCA ACA TCG AGG Arg Pro Pro Leu Pro Ala Val * Gln Arg Pro Thr Pro Thr Ser Arg 65 70 75	238
AAG TGG CCC TGC CTC AGG AGG GGG AGG TTC CCT TCT ACG GCA GAG CCA Lys Trp Pro Cys Leu Arg Arg Gly Arg Phe Pro Ser Thr Ala Glu Pro 80 85 90 95	286
TTC CCC TTG CTT TTA TAA AGG GTG GTA GGC ATC TCA TCT TCT GCC ATT Phe Pro Leu Leu Leu * Arg Val Val Gly Ile Ser Ser Ser Ala Ile 100 105 110	334
CCA AGA AAA AAT GTG ATG AAC TCG CCA AGC AAC TGA CCA GCC TGG GCG Pro Arg Lys Asn Val Met Asn Ser Pro Ser Asn * Pro Ala Trp Ala 115 120 125	382
TGA ACG CCG TGG CAT ATT ATA GAG GTC TAG ACG TCG CCG TCA TAC CCA * Thr Pro Trp His Ile Ile Glu Val * Thr Ser Pro Ser Tyr Pro 130 135 140	430
CAA CAG GAG ACG TGG TCG TGT GCA GCA CCG ACG CGC TCA TGA CGG GAT Gln Gln Glu Thr Trp Ser Cys Ala Ala Pro Thr Arg Ser * Arg Asp 145 150 155	478
TCA CCG GCG ACT TTG ATT CTG TCA TAG ACT GCA ACT CCG CCG TCA CTC Ser Pro Ala Thr Leu Ile Leu Ser * Thr Ala Thr Pro Pro Ser Leu 160 165 170 175	526
AGA CGG TGG ACT TCA GTC TGG ATC CCA CTT TTA CCA TTG AGA CTA CCA Arg Arg Trp Thr Ser Val Trp Ile Pro Leu Leu Pro Leu Arg Leu Pro 180 185 190	574
CAG TGC CCC AGG ACG CAG TGT CCA GAA GCC AGC GTT GGG GCC GCA CGG Gln Cys Pro Arg Thr Gln Cys Pro Glu Ala Ser Val Gly Ala Ala Arg 195 200 205	622
GGA GAG GTA GGC ACG GCA TAT ACC GGT ATG TCT CGG CTG GAG AGA GAC Gly Glu Val Gly Thr Ala Tyr Thr Gly Met Ser Arg Leu Glu Arg Asp 210 215 220	670
CGT CTG GCA TGT TCG ACT CCG TGG TGC TCT GTG AGT GCT ACG ATG CCG Arg Leu Ala Cys Ser Thr Pro Trp Cys Ser Val Ser Ala Thr Met Pro	718

225	230	235	
GAT GTG CAT GGT ACG ATC TGA CTC CTG CCG AGA CTA CCG TGA GGT TGC Asp Val His Gly Thr Ile * Leu Leu Pro Arg Leu Pro * Gly Cys 240 245 250 255			766
GCG CTT ACT AAA CAC CCC CGG GCT CCC TGT CTG TCA GGA CCA TTT GGA Ala Leu Thr Lys His Pro Arg Ala Pro Cys Leu Ser Gly Pro Phe Gly 260 265 270			814
ATT CTG GGA GGG GGT GTT CAC GGG GCT CAC TAA CAT CGA CGC TCA CAT Ile Leu Gly Gly Gly Val His Gly Ala His * His Arg Arg Ser His 275 280 285			862
GCT GTC ACA GAC CAA ACA GGG TGG GGA GAA TTT CCC ATA CCT TGT AGC Ala Val Thr Asp Gln Thr Gly Trp Gly Glu Phe Pro Ile Pro Cys Ser 290 295 300			910
GTA CCA AGC AAC AGT CTG TGT TCG CGC GAA AGC GCC CCC CCC CAG CTG Val Pro Ser Asn Ser Leu Cys Ser Arg Glu Ser Ala Pro Pro Gln Leu 305 310 315			958
GGA CAC AAT GTG GAA ATG CAT GCT CCG TCT CAA ACC GAC TTA ACT GGC Gly His Asn Val Glu Met His Ala Pro Ser Gln Thr Asp Leu Thr Gly 320 325 330 335			1006
CCT ACT CCC CTC TTG TAC AGG CTG GGG CCC GTC CAG AAT GAG ATC ACA Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile Thr 340 345 350			1054
CTG ACG CAC CCC ATC ACC AAG TAC ATT ATG GCT TGC ATG TCT GCG GAC Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp 355 360 365			1102
TTG GAG GTC ATT ACC AGC ACT TGG GTT CTG GTG GGG GGC GTT GTG GCG Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly Gly Val Val Ala 370 375 380			1150
GCC CTG GCG GCC TAC TGC TTG ACG GTG GGT TCG GTA GCC ATA GTC GGT Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val Ala Ile Val Gly 385 390 395			1198
AGG ATC ATC CTC TCT GGG AAA CCT GCC ATC ATT CCC GAT AGG GAG GTA Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Val 400 405 410 415			1246
TTA TAC CAG CAA TTT GAT GAG ATG GAG GAG TGC TCG GCC TCG TTG CCC Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser Ala Ser Leu Pro 420 425 430			1294
TAT ATG GAC GAA ACA CGT GCC ATT GCC GGA CAA TTC AAA GAG AAA GTG Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe Lys Glu Lys Val 435 440 445			1342
CTC GGC TTC ATC AGC ACG ACC GGC CAG AAG GCT GAA ACT CTG AAG CCG Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu Thr Leu Lys Pro 450 455 460			1390

GCA GCC ACG TCT GTG TGG AAC AAG GCT GAG CAG TTC TGG CCA CAT ACA 1438
 Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe Trp Pro His Thr
 465 470 475

TGT GGA ACT TCA TCA GTG GGA TAC AAT AAT AG 1470
 Cys Gly Thr Ser Ser Val Gly Tyr Asn Asn
 480 485

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

TGTGCCAGGA CCATCACCAC CGGAGCTTCT ATCATACTACT CCACCTACGG CAAGTTCCTT 60
 GCTGATGGAG GGTGTTTCAG CGCGCGCAT GACGTGATCA TATGCGACGA GTGCCATTCC 120
 CAGGACGCCA CCACCATTTT TGGGATAGGC ACTGTCCTTG ACCAGGCAGA GACGGCTGGA 180
 GCTAGGCTCG TGTCTTGGC CACGCGCACC CCTCCCGSCA GTGTGACAAC GCCCCACCCC 240
 AACATCGAGG AAGTGGCCCT GCCTCAGGAG GGGGAGGTTT CCTTCTACGG CAGAGCCATT 300
 CCCCTTGCTT TTATAAAGGG TGGTAGGCAT CTCATCTTCT GCCATTCCAA GAAAAATGT 360
 GATGAACCTG CCAAGCAACT GACCAGCCTG GCGTGAACG CCGTGGCATA TTATAGAGGT 420
 CTAGACGTCG CCGTCATACC CACAACAGGA GACGTGGTCG TGTGCAGCAC CGACGCGCTC 480
 ATGACGGGAT TCACCGCGCA CTTTGATTCT GTCATAGACT GCAACTCCGC CGTCACTCAG 540
 ACGGTGGACT TCAGTCTGGA TCCCACCTTT ACCATTGAGA CTACCACAGT GCCCCAGGAC 600
 GCAGTGTCCA GAAGCCAGCG TTGGGGCCGC ACGGGGAGAG GTAGGCACGG CATATACCGG 660
 TATGTCTCGG CTGGAGAGAG ACCGTCTGGC ATGTTGCACT CCGTGGTGCT CTGTGAGTGC 720
 TACGATGCCG GATGTGCATG GTACGATCTG ACTCTTGCCG AGACTACCGT GAGGTGCGC 780
 GCTTACNTAA ACACCCCGCG GCTCCCTGTC TGTGAGGACC ATTGGAATT CTGGAGGGGG 840
 GTGTTACGGG GGCTCACTAA CATCGACGCT CACATGCTGT CACAGACCAA ACAGSGTGGG 900
 GAGATTTC CATACTTGT AGCGTACCAA GCAACAGTCT GTGTTGCGCG GAAAGCGCCC 960

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CCCCCAGCT GGGACACAAT GTGGAAATGC ATGCTCCGTC TCAAACCGAC NTTAACTGGC 1020
CCTACTCCCC TCTGTACAG GCTGGGGCCC GTCCAGAATG AGATCACACT GACGCACCCC 1080
ATCACCAAGT ACATTATGGC TTGCATGTCT GCGGACTTGG AGGTCAATTAC CAGCACTTGG 1140
GTTCTGTGTG GGGGCGTTGT GCGGCGCCTG GCGGCCTACT GCTTGACGGT GGGTTCGGTA 1200
GCCATAGTCG GTAGGATCAT CCTCTCTGGG AAACCTGCCA TCATTCCCGA TAGGGAGGTA 1260
TTATACCAGC AATTGTATGA GATGGAGGAG TGCTCGGCCT CGTTGCCCTA TATGGACGAA 1320
ACACGTGCCA TTGCGGACA ATTCAAAGAG AAAGTGCTCG GCTTCATCAG CACGACCGGC 1380
CAGAAGGCTG AAACCTGAA GCGGCGAGCC ACGTCTGTGT GGAACAAGGC TGAGCAGTTC 1440
TGNCCACAT ACATGTGAA CTTCATCAGT GGGATACAAT AATAG 1485

```

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 484 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

```

Cys Ala Arg Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr
1           5           10           15

Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala His Asp Val
20           25           30

Ile Ile Cys Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly
35           40           45

Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val
50           55           60

Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro
65           70           75           80

Asn Ile Glu Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr
85           90           95

Gly Arg Ala Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile
100          105          110

Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr
115          120          125

Ser Leu Gly Val Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ala
130          135          140

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Val Ile Pro Thr Thr Gly Asp Val Val Val Cys Ser Thr Asp Ala Leu			
145	150	155	160
Met Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser			
165	170		175
Ala Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile			
180	185		190
Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Trp			
195	200	205	
Gly Arg Thr Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala			
210	215	220	
Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Val Val Leu Cys Glu Cys			
225	230	235	240
Tyr Asp Ala Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr			
245	250		255
Val Arg Leu Arg Ala Tyr Xaa Asn Thr Pro Gly Leu Pro Val Cys Gln			
260	265		270
Asp His Leu Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile			
275	280		285
Asp Ala His Met Leu Ser Gln Thr Lys Gln Gly Gly Glu Asn Phe Pro			
290	295	300	
Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro			
305	310	315	320
Pro Pro Ser Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro			
325	330		335
Xaa Leu Thr Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln			
340	345		350
Asn Glu Ile Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys			
355	360		365
Met Ser Ala Asp Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly			
370	375		380
Gly Val Val Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val			
385	390	395	400
Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro			
405	410		415
Asp Arg Glu Val Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser			
420	425		430
Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe			
435	440		445

Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu
450 455 460

Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe
465 470 475 480

Trp Xaa Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 199:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1485 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

TGTGCCAGGA CCATCACCAC CGGAGCTTCT ATCACATACT CCACTTACGG CAAGTTCCTT	60
GCTGATGGAG GGTGTTTCAGG CGGCGCGTAT GACGTGATCA TATGCGACGA GTGCCATTCC	120
CAGGACGCCA CCACCATCTT TGGGATAGGC ACTGTCCTTG ACCAGGCAGA GACGGCTGGA	180
GCTAGGCTCG TCGTCTTGCC CACGGCCACC CCTCCCGGCA GTGTGACAAC GCCCCACCCC	240
AACATCGAGG AAGTGGCCCT GCCTCAGGAG GGGGAGGTTT CCTTCTACGG CAGAGCCATT	300
CCCCTTGCTT TTATAAAGGG TGGTAGGCAT CTCATCTTCT GCCATTCCAA GAAAAAATGT	360
GATGAATCG CCAAGCAACT GACCAGCCTG GCGGTGAACG CCGTGGCATA TTATAGAGGT	420
CTAGACGTCT CCGTCATCCC CACAGCAGGA GACGTGGTCG TGTGCAGCAC CGACGCGCTC	480
ATGACGGGAT TCACCGCGGA CTTTGATTCT GTCATAGACT GCAACTCCGC CGTCACTCAG	540
ACGGTGGACT TCAGTCTGGA TCCCACTTTT ACCATTGAGA CTACCACAGT GCCCCAGGAC	600
GCAGTGTCGA GAAGCCAGCG TAGGGGCGCG ACGGGGAGAG GTAGGCACGG CATATACCGG	660
TATGTCTTCG CTGGAGAGAG ACCNCTGAC ATGTTGACT CCGTGGTCT CTGTGAGTGC	720
TACGATGCCG GATGTGCGTG GTATGATCTG ACTCCTGCCG AGACTACCGT GAGGTGCGC	780
GCTTACATAA ACACCCCGGG GCTCCCTGTC TGTGAGACC ATTTGGAATT CTGGGAGGGG	840
GTGTTACCGG GGCTCACTAA CATCGACGCT CACATGCTGT CACAGACCAA ACAGGGTGGG	900
GAGAATTTC CATACCTTGT AGCGTACCAA GCAACAGTCT GTGTTGCGCG GAAAGCGCCC	960

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CCCCCAGCT GGGACACAAT GTGGAAATGC ATGCTCOGTC TCAAACCGAC TTTAACTGGC 1020
CCTACTCCCC TCTGTACAG GCTGGGGCCC GTCCAGANTG AGATCACACT GACGCACCCC 1080
ATCACCAAGT ACATTATGGC TTGCATGICT GCGGACTTGG AGGTCAATTAC CANCACTTGG 1140
GTTCTGGTGG GGGGCGTTGT GCGGCGCCTG GCGGCCTACT GCTTGACGCT GGGTTCGGTA 1200
GOCATAGTCG GTAGGATCAT CCTCTCTGGG AAACCTGCCA TCATTCCCAG TAGGGAGGCA 1260
TTATACCAGC AATTGTATGA GATGGAGGAG TGCTCGGCCT CGTTGCCCTA TATGGACGAG 1320
ACACGTGCCA TTCCCGGACA ATTCMAAGAG AAGTGCTCG GCTTCATCAG CACGACCGGC 1380
CAGAAGGCTG AAACCTGTAA GCCGGCAGCC ACGTCTGTGT GGAACAAGGC TGAGCAGTTC 1440
TGGGCCACAT ACATGTGGAA CTTTCATCAG GGGATACAAT AATAG 1485

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(2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

```

Cys Ala Arg Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr
1           5           10           15
Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val
20          25          30
Ile Ile Cys Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly
35          40          45
Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val
50          55          60
Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro
65          70          75          80
Asn Ile Glu Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr
85          90          95
Gly Arg Ala Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile
100         105         110
Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr
115         120         125

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Ser Leu Gly Val Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ala
 130 135 140
 Val Ile Pro Thr Ala Gly Asp Val Val Val Cys Ser Thr Asp Ala Leu
 145 150 155 160
 Met Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser
 165 170 175
 Ala Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile
 180 185 190
 Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg
 195 200 205
 Gly Arg Thr Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala
 210 215 220
 Gly Glu Arg Xaa Ser Asp Met Phe Asp Ser Val Val Leu Cys Glu Cys
 225 230 235 240
 Tyr Asp Ala Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr
 245 250 255
 Val Arg Leu Arg Ala Tyr Ile Asn Thr Pro Gly Leu Pro Val Cys Gln
 260 265 270
 Asp His Leu Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile
 275 280 285
 Asp Ala His Met Leu Ser Gln Thr Lys Gln Gly Gly Glu Asn Xaa Pro
 290 295 300
 Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro
 305 310 315 320
 Pro Pro Ser Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro
 325 330 335
 Thr Leu Thr Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln
 340 345 350
 Xaa Glu Ile Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys
 355 360 365
 Met Ser Ala Asp Leu Glu Val Ile Thr Xaa Thr Trp Val Leu Val Gly
 370 375 380
 Gly Val Val Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val
 385 390 395 400
 Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro
 405 410 415
 Asp Arg Glu Ala Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser
 420 425 430
 Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe

435	440	445
Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu		
450	455	460
Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe		
465	470	480

Trp Ala Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 201:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

C TCC ACT GTG ACT GAG AGA GAC ATC AGG GTC GAA GAA GAA GTC TAT	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAT CTG GAG CCC GAG GCC CGC AAG GTA ATA ACC GCC CTC	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu	
20 25 30	
ACG GAG AGA CTC TAC GTG GGC GGC CCT ATG TAC AAT AGC AAG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp	
35 40 45	
CTT TGC GGG TAT CGC AGG TGC CGC GCA AGC GGC GTA TAT ACC ACC AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACA CTG ACG TGC TAC CTT AAA GCC TCA GCA GCC ATC AGG	238
Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg	
65 70 75	
GCT GCG GGG CTG AAG GAC TGC ACC ATG CTG GTT TGC GGT GAC GAC TTA	286
Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	

GTC GTG ATC GCT GAA AGC GGT GGC GTC GAG GAG GAC AAG CGA GCC CTC 334
 Val Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu
 100 105 110

GGA GCT 340
 Gly Ala

(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr Gln
 1 5 10 15
 Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr
 20 25 30
 Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu
 35 40 45
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
 50 55 60
 Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala
 65 70 75 80
 Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95
 Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
 100 105 110
 Ala

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..340

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

C TCC ACA GTG ACT GAA AGA GAC ATC AGG GTC GAG GAA GAG GTC TAC	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAC CTG GAG CCT GAA ACC CGC AAG GTA ATA TCT GCC CTC	94
Gln Cys Cys Asp Leu Glu Pro Glu Thr Arg Lys Val Ile Ser Ala Leu	
20 25 30	
ACT GAA AGA CTC TAT GTG GGC GGT CCC ATG CAC AAC AGC AGG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Arg Gly Asp	
35 40 45	
CTA TGC GGG TAC CGT AGA TGC CGC GCG AGC GGC GTA TAC ACC ACA AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACT CTG ACG TGC TTC CTC AAG GCC ACA GCG GCC ACC AAA	238
Phe Gly Asn Thr Leu Thr Cys Phe Leu Lys Ala Thr Ala Thr Lys	
65 70 75	
GCC GCT GGC CTA AAG GAC TGC ACC ATG TTG GTG TGT GGT GAC GAC TTA	286
Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTC GTT ATC GCC GAA AGC GAT GGT GTC GAA GAG GAC CGC CGA GCC CTC	334
Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Arg Arg Ala Leu	
100 105 110	
GGA GCT	340
Gly Ala	

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr Gln
1 5 10 15

```

Cys Cys Asp Leu Glu Pro Glu Thr Arg Lys Val Ile Ser Ala Leu Thr
      20                      25                      30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Arg Gly Asp Leu
      35                      40                      45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
      50                      55                      60

Gly Asn Thr Leu Thr Cys Phe Leu Lys Ala Thr Ala Ala Thr Lys Ala
      65                      70                      75                      80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
      85                      90                      95

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Arg Arg Ala Leu Gly
      100                      105                      110

```

Ala

(2) INFORMATION FOR SEQ ID NO: 205:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..340

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

```

C TCC ACG GTG ACC GAA AGG GAT ATC AGG ACC GAG GAA GAG ATC TAC      46
  Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr
    1                      5                      10                      15

CAG TGC TGC GAC CTG GAG CCC GAA GCC CGC AAG GTG ATA TCC GCC CTA      94
  Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu
    20                      25                      30

ACG GAA AGA CTC TAC GTG GGC GGT CCC ATG TAC AAC TCC AAG GGG GAC      142
  Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp
    35                      40                      45

```

262

CTA TGC GGG CAA CGG AGG TGC CGC GCA AGC GGG GTC TAC ACC ACC AGC	190
Leu Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Ser	
50 55 60	
TTC GGG AAC ACT GTA ACG TGT TAT CTC AAG GCC GTT GCG GCT ACT AGG	238
Phe Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Thr Arg	
65 70 75	
GCC GCA GGT CTG AAA GGT TGC AGC ATG CTG GTT TGT GGA GAC GAC TTA	286
Ala Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTC GTC ATC TGC GAG AGC GGC GGC GTA GAG GAG GAT GCA AGA GCC CTC	334
Val Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu	
100 105 110	
CGA GCC	340
Arg Ala	

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr Gln	
1 5 10 15	
Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu Thr	
20 25 30	
Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu	
35 40 45	
Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe	
50 55 60	
Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Thr Arg Ala	
65 70 75 80	
Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val	
85 90 95	
Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu Arg	
100 105 110	
Ala	

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

C TCC ACG GTG ACT GAA AGG GAC ATT AGG GTC GAG GAA GAG ATC TAC	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Ile Tyr	
1 5 10 15	
CAG TGC TGT GAC CTG GAG CCC GAG GCA CGC AAG GTG ATA TCC GCT CTC	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu	
20 25 30	
ACA GAA AGA CTC TAC AAG GGC GGC CCC ATG TAT AAC AGC AAG GGG GAC	142
Thr Glu Arg Leu Tyr Lys Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp	
35 40 45	
CTA TGC GGG CTT CGG AGG TGC CGC GCA AGC GGG GTA TAC ACC ACA AGC	190
Leu Cys Gly Leu Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACG GTG ACA TGC TAC CTT AAA GCC ACA GCA GCC ACC AGG	238
Phe Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Thr Ala Thr Arg	
65 70 75	
GCT GCA GGG CTG AAA GAT TGC ACT ATG CTG GTA TGC GGT GAC GAC TTA	286
Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTC GTT ATT GCC GAA AGC GGT GGC GTG GAG GAG GAC GCC CGA GCC CTC	334
Val Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu	
100 105 110	
CGA GCC	340
Arg Ala	

(2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

```

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Ile Tyr Gln
 1             5             10             15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu Thr
                20             25             30

Glu Arg Leu Tyr Lys Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu
        35             40             45

Cys Gly Leu Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
        50             55             60

Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala
        65             70             75             80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
        85             90             95

Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu Arg
        100            105            110

```

Ala

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

```

CCCCACCGTG ACNAGAGAGG ACNTCAGGGT CGAGGAAGAG GTCTATCAGT GCTGTAATCT      60
GGAGNCCGAT GNC CGCARG TCATCAACGC CCTCACAGAG AGACTCTACG TGGGCGGCC      120

```

TATGCACAAC AGCAAGGGAG ACCTGTGTGG CATCCGTAGA TGCCGCGCGA GCGGCGTTTA	180
CACCACGAGC TTCGGAACA CGCTGACTTG CTACCTCAA GCCACAGCG CCACCAGGGC	240
CGCGGGCTTG AAGGATTGCA CCATGCTGGT CTGCGGNGAC GACCTGGTTG TCATTGCTGA	300
GAGCATTGGC ATAGACGAGG ACAAGCAAGC CCTCCGNACT	340

(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

Pro Thr Val Thr Glu Arg Asp Xaa Arg Val Glu Glu Glu Val Tyr Gln		
1	5	10 15
Cys Cys Asn Leu Glu Xaa Asp Xaa Arg Lys Val Ile Asn Ala Leu Thr		
20	25	30
Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu		
35	40	45
Cys Gly Ile Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Ser Phe		
50	55	60
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala		
65	70	75 80
Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val		
85	90	95
Val Ile Ala Glu Ser Ile Gly Ile Asp Glu Asp Lys Gln Ala Leu Arg		
100	105	110
Thr		

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

CTCGACTGTG NCCGAGAGGG ACATCAGGAC AGAGGGAGAG GTCTATCAGT GTTGCACCT	60
GGAACCGGAA GCCCGCAAGG TAATCACCGC CCTCACTGAG AGACTCTATG TGGGCGGACC	120
CATGTTCAAC AGCAAGGGAG ACCTGTGCGG ACACGCCCGG TSCCGCGCAA GCGGCGTGTT	180
CACCACCAGC TTCGGGAACA CACTGACGTG CTACCTTAAA GCCACAGCTG CTACTAGAGC	240
AGCCGGCTTA AAAGATTGCA CCATGCTGGT CTGCGGTGAC GACTTAGTCG TTATTCCGA	300
GAGCGCCGGT GTGGAGGAGG ATCCCANAA C NNCGACCN	340

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

Ser Thr Val Xaa Glu Arg Asp Ile Arg Thr Glu Gly Glu Val Tyr Gln	
1 5 10 15	
Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr	
20 25 30	
Glu Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly Asp Leu	
35 40 45	
Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Phe	
50 55 60	
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala	

65	70	75	80
Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val			
85		90	95
Val Ile Ser Glu Ser Ala Gly Val Glu Glu Asp Pro Xaa Thr Xaa Arg			
100	105	110	

Pro

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

C TCA ACA GTC ACC GAG AAC GAC ATC CGT GTT GAG GAG TCA ATT TAC	46
Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Ser Ile Tyr	
1 5 10 15	
CAA TGT TGT GAC TTG GCC CCC GAG GCC AGA CAG GCC ATA AAG TCG CTC	94
Gln Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Lys Ser Leu	
20 25 30	
ACA GAG CGG CTT TAT ATC GGG GGT CCC CTG ACT AAT TCA AAG GGG CAG	142
Thr Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln	
35 40 45	
AAC TGT GGC TAT CGC CGA TGC CGC GCA AGC GGC GTG CTG ACG ACC AGC	190
Asn Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser	
50 55 60	
TGC GGT AAT ACC CTT ACA TGT TAC CTA AAG GCC TCT GCA GCC TGT CGA	238
Cys Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys Arg	
65 70 75	
GCT GCG AAG CTC CAG GAC TGC ACG ATG CTC GTG TGC GGG GAC GAC CTT	286

Ala	Ala	Lys	Leu	Gln	Asp	Cys	Thr	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu		
80					85				90						95		
GTC	GTT	ATC	TGT	GAA	AGC	GCG	GGA	ACC	CAA	GAG	GAC	GCG	GCG	AGC	CTA	334	
Val	Val	Ile	Cys	Glu	Ser	Ala	Gly	Thr	Gln	Glu	Asp	Ala	Ala	Ser	Leu		
			100					105					110				
CGA	GTC															340	
Arg	Val																

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

Ser	Thr	Val	Thr	Glu	Asn	Asp	Ile	Arg	Val	Glu	Glu	Ser	Ile	Tyr	Gln		
1				5				10					15				
Cys	Cys	Asp	Leu	Ala	Pro	Glu	Ala	Arg	Gln	Ala	Ile	Lys	Ser	Leu	Thr		
		20						25					30				
Glu	Arg	Leu	Tyr	Ile	Gly	Gly	Pro	Leu	Thr	Asn	Ser	Lys	Gly	Gln	Asn		
		35					40					45					
Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Thr	Thr	Ser	Cys		
	50					55					60						
Gly	Asn	Thr	Leu	Thr	Cys	Tyr	Leu	Lys	Ala	Ser	Ala	Ala	Cys	Arg	Ala		
	65				70			75					80				
Ala	Lys	Leu	Gln	Asp	Cys	Thr	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val		
			85					90						95			
Val	Ile	Cys	Glu	Ser	Ala	Gly	Thr	Gln	Glu	Asp	Ala	Ala	Ser	Leu	Arg		
		100						105					110				
Val																	

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..340

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

C TCA ACC GTC ACG GAG AGG GAT ATA AGA ACA GAA GAA TCC ATA TAT	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr	
1 5 10 15	
CAA GCT TGT TCC CTG CCC CAA GAG GCC AGA ACT GTC ATA CAC TCG CTC	94
Gln Ala Cys Ser Leu Tyr Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu	
20 25 30	
ACC GAG AGA CTC TAC GTG GGA GGG CCC ATG ATA AAC AGC AAA GGG CAA	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Ile Asn Ser Lys Gly Gln	
35 40 45	
TCC TGC GGT TAC AGG CGT TGC CGC GCA AGC GGT GTT TTC ACC ACC AGC	190
Ser Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser	
50 55 60	
ATG GGG AAT ACC ATG ACG TGT TAC ATC AAA GCC CTT GCA GCG TGT AAA	238
Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys	
65 70 75	
GCC GCA GGG ATC GTG GAC CCC GTC ATG CTG GTG TGT GGA GAC GAC CTG	286
Ala Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTC GTC ATC TCG GAG AGC CAG GGT AAC GAG GAG GAC GAG CGA AAC CTG	334
Val Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu Arg Asn Leu	
100 105 110	
AGA GCT	340
Arg Ala	

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

```

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Gln
 1              5              10              15

Ala Cys Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu Thr
 20              25              30

Glu Arg Leu Tyr Val Gly Gly Pro Met Ile Asn Ser Lys Gly Gln Ser
 35              40              45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met
 50              55              60

Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys Ala
 65              70              75              80

Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val
 85              90              95

Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu Arg Asn Leu Arg
100              105              110

```

Ala

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

```

C TCG ACT GTC ACT GAA CAG GAC ATC AGG GTG GAA GAG GAG ATA TAT      46
Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile Tyr
 1              5              10              15

CAA TGC TGC AAC CTT GAA CCG GAG GCC AGG AAA GTG ATC TCC TCC CTC      94
Gln Cys Cys Asn Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ser Leu

```

20	25	30	
ACG GAG CGG CTT TAC TGC GGA GGC CCT ATG TTT AAC AGC AAG GGG GCC			142
Thr Glu Arg Leu Tyr Cys Gly Gly	Pro Met Phe Asn Ser Lys Gly Ala		
35	40	45	
CAG TGT GGT TAT CGC CGT TGC CGT GCC AGT GGA GTT CTG CCT ACC AGC			190
Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser			
50	55	60	
TTT GGC AAC ACA ATC ACT TGT TAC ATC AAG GCC ACA ACG GCC GCG AAG			238
Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Thr Ala Ala Lys			
65	70	75	
GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTC TGC GGA GAT GAT CTG			286
Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp Leu			
80	85	90	95
GTC GTG GTG GCT GAG AGT GAT GGC GTC GAC GAG GAT AGA GCA GCC CTG			334
Val Val Val Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Ala Ala Leu			
100	105	110	
AGA GCC			340
Arg Ala			

(2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln			
1	5	10	15
Cys Cys Asn Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ser Leu Thr			
20	25	30	
Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Ala Gln			
35	40	45	
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Phe			
50	55	60	
Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Thr Ala Ala Lys Ala			
65	70	75	80
Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp Leu Val			
85	90	95	
Val Val Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Ala Ala Leu Arg			
100	105	110	

Ala

(2) INFORMATION FOR SEQ ID NO: 219:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

Arg	Ser	Glu	Gly	Arg	Thr	Ser	Trp	Ala	Gln
1				5					10

(2) INFORMATION FOR SEQ ID NO: 220:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

Arg	Ser	Glu	Gly	Arg	Thr	Ser	Trp	Ala	Gln
1				5					10

(2) INFORMATION FOR SEQ ID NO: 221:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

Arg	Thr	Glu	Gly	Arg	Thr	Ser	Trp	Ala	Gln
1				5					10

(2) INFORMATION FOR SEQ ID NO: 222:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 629 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 3..629

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 3..629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

TA GAC TTT TGS GAG AGC GTC TTC ACT GGA CTA ACT CAC ATA GAT GCC	47
Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala	
1 5 10 15	
CAC TTT CTG TCA CAG ACT AAG CAG CAG GGA CTC AAC TTC TCG TTC CTG	95
His Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu	
20 25 30	
ACT GCC TAC CAA GCC ACT GTG TGC GCT CGC GCG CAG GCT CCT CCC CCA	143
Thr Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro	
35 40 45	
AGT TGG GAC GAG ATG TGG AAG TGT CTC GTA CGG CTT AAG CCA ACA CTA	191
Ser Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu	
50 55 60	
CAT GGA CCT ACG CCT CTT CTA TAT CGG TTG GGG CCT GTC CAA AAT GAA	239
His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu	
65 70 75	
ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG GCA TGC ATG TCA	287
Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser	
80 85 90 95	
GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG CTT GGA GGG GTC	335
Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu Gly Gly Val	
100 105 110	
CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT TGT GTT GTG ATT	383
Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys Val Val Ile	
115 120 125	
GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC GTT CCA GAC AAA	431
Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val Pro Asp Lys	
130 135 140	

GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG TGC TCA CAA GCT	479
Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys Ser Gln Ala	
145 150 155	
GCC CCA TAT ATC GAA CAA GCT CAG GTA RTA GCT CAC CAG TTC AAG GAA	527
Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln Phe Lys Glu	
160 165 170 175	
AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA CAA GCT GTC ATT	575
Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Ala Val Ile	
180 185 190	
GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG GCC TTT TGG CAC	623
Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala Phe Trp His	
195 200 205	
AAG CAT	629
Lys His	

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His	
1 5 10 15	
Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu Thr	
20 25 30	
Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser	
35 40 45	
Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu His	
50 55 60	
Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile	
65 70 75 80	
Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala	
85 90 95	
Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu Gly Gly Val Leu	
100 105 110	
Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys Val Val Ile Val	
115 120 125	
Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val Pro Asp Lys Glu	
130 135 140	

Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys Ser Gln Ala Ala
 145 150 155 160

Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln Phe Lys Glu Lys
 165 170 175

Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln Ala Val Ile Glu
 180 185 190

Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala Phe Trp His Lys
 195 200 205

His

(2) INFORMATION FOR SEQ ID NO: 224:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 2..12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

Ile His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 225:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

Val	Asn	Tyr	Arg	Asn	Ala	Ser	Gly	Val	Tyr	His	Ile
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

Val	Asn	Tyr	His	Asn	Thr	Ser	Gly	Ile	Tyr	His	Leu
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

Gln	His	Tyr	Arg	Asn	Ala	Ser	Gly	Ile	Tyr	His	Val
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

Ile His Tyr Arg Asn Ala Ser Asp Gly Tyr Tyr Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

Leu Gln Val Lys Asn Thr Ser Ser Ser Tyr Met Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

Val Trp Gln Leu Arg Ala Ile Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

Val	Tyr	Glu	Ala	Asp	Tyr	His	Ile	Leu	His	Leu
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

Val	Tyr	Glu	Thr	Asp	Asn	His	Ile	Leu	His	Leu
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 235:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

Val	Tyr	Glu	Thr	Glu	Asn	His	Ile	Leu	His	Leu
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 236:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

Val Phe Glu Thr Val His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

Val Phe Glu Thr Glu His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

Val Phe Glu Thr Asp His His Ile Met His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

Val Tyr Glu Thr Glu Asn His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 240:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

Val Tyr Glu Ala Asp Ala Leu Ile Leu His Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 241:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

Val Gln Asp Gly Asn Thr Ser Ala Cys Trp Thr Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 243:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 244:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

Val Arg Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 245:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Ile Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 246:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Ile Ala Leu

1 5 10

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

Val Lys Thr Gly Asn Ser Val Arg Cys Trp Ile Pro Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

Val Lys Thr Gly Asn Val Ser Arg Cys Trp Ile Ser Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

Val Arg Lys Asp Asn Val Ser Arg Cys Trp Val Gln Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

Ala Pro Ser Phe Gly Ala Val Thr Ala Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

Val Ser Gln Pro Gly Ala Leu Thr Lys Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

Val Lys Tyr Val Gly Ala Thr Thr Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

Ala Pro Tyr Ile Gly Ala Pro Val Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 254:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

Ala Gln His Leu Asn Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 255:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

Ser Pro Tyr Val Gly Ala Pro Leu Glu Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 256:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

Ser Pro Tyr Ala Gly Ala Pro Leu Glu Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

Ala	Pro	Tyr	Leu	Gly	Ala	Pro	Leu	Glu	Ser
1				5				10	

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

Ala	Pro	Tyr	Leu	Gly	Ala	Pro	Leu	Glu	Ser
1				5				10	

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

Ala	Pro	Tyr	Val	Gly	Ala	Pro	Leu	Glu	Ser
1				5				10	

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

Asn Val Pro Tyr Leu Gly Ala Pro Leu Thr Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

Ala Pro His Leu Arg Ala Pro Leu Ser Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

Ala Pro Tyr Leu Gly Ala Pro Leu Thr Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

Arg Pro Arg Gln His Ala Thr Val Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 264:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

Ser	Pro	Gln	His	His	Lys	Phe	Val	Gln	Asp
1				5					10

(2) INFORMATION FOR SEQ ID NO: 265:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

Arg	Pro	Arg	Arg	Leu	Trp	Thr	Thr	Gln	Glu
1				5					10

(2) INFORMATION FOR SEQ ID NO: 266:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

Pro	Pro	Arg	Ile	His	Glu	Thr	Thr	Gln	Asp
1				5					10

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

Thr Ile Ser Tyr Ala Asn Gly Ser Gly Pro Ser Asp Asp Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

Ser Arg Arg Gln Pro Ile Pro Arg Ala Arg Arg Thr Glu Gly Arg Ser
1 5 10 15

Trp Ala Gln

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1443

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

ACC ATC ACC ACC GGA GCT TCT ATC ACA TAC TCC ACT TAC GGC AAG TTC
Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe

48

1	5	10	15	
CTT GCT GAT GGA GGG TGT TCA GGC GGC GCG TAT GAC GTG ATC ATA TGC				96
Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val Ile Ile Cys				
20		25	30	
GAC GAG TGC CAT TCC CAG GAC GCC ACC ACC ATT CTT GGG ATA GGC ACT				144
Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr				
35		40	45	
GTC CTT GAC CAG GCA GAG ACG GCT GGA GCT AGG CTC GTC GTC TTG GCC				192
Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala				
50		55	60	
ACG GCC ACC CCT CCC GGC AGT GTG ACA ACG CCC CAC CCC AAC ATC GAG				240
Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn Ile Glu				
65		70	75	80
GAA GTG GCC CTG CCT CAG GAG GGG GAG GTT CCC TTC TAC GGC AGA GCC				288
Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Gly Arg Ala				
85		90	95	
ATT CCC CTT GCT TTT ATA AAG GGT GGT AGG CAT CTC ATC TTC TGC CAT				336
Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His				
100		105	110	
TCC AAG AAA AAA TGT GAT GAA CTC GCC AAG CAA CTG ACC AGC CTG GGC				384
Ser Lys Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr Ser Leu Gly				
115		120	125	
GTG AAC GCC GTG GCA TAT TAT AGA GGT CTA GAC GTC GCC GTC ATC CCC				432
Val Asn Ala Val Val Tyr Tyr Arg Gly Leu Asp Val Ala Val Ile Pro				
130		135	140	
ACA GCA GGA GAC GTG GTC GTG TGC AGC ACC GAC GCG CTC ATG ACG GGA				480
Thr Ala Gly Asp Val Val Val Cys Ser Thr Asp Ala Leu Met Thr Gly				
145		150	155	160
TTC ACC GGC GAC TTT GAT TCT GTC ATA GAC TGC AAC TCC GCC GTC ACT				528
Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser Ala Val Thr				
165		170	175	
CAG ACG GTG GAC TTC AGT CTG GAT CCC ACT TTT ACC ATT GAG ACT ACC				576
Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr				
180		185	190	
ACA GTG CCC CAG GAC GCA GTG TCC AGA AGC CAG CGT AGG GGC GCG ACG				624
Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr				
195		200	205	
GGG AGA GGT AGG CAC GGC ATA TAC CGG TAT GTC TCG GCT GGA GAG AGA				672
Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala Gly Glu Arg				
210		215	220	
CCG TCT GAC ATG TTC GAC TCC GTG GTG CTC TGT GAG TGC TAC GAT GCC				720
Pro Ser Asp Met Phe Asp Ser Val Val Leu Cys Glu Cys Tyr Asp Ala				
225		230	235	240

290

GGA TGT GCG TGG TAT GAT CTG ACT CCT GCC GAG ACT ACC GTG AGG TTG Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr Val Arg Leu 245 250 255	768
CGC GCT TAC ATA AAC ACC CCC GGG CTC CCT GTC TGT CAG GAC CAT TTG Arg Ala Tyr Ile Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu 260 265 270	816
GAA TTC TGG GAG GGG GTG TTC ACG GGG CTC ACT AAC ATC GAC GCT CAC Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile Asp Ala His 275 280 285	864
ATG CTG TCA CAG ACC AAA CAG GGT GGG GAG AAT TTC CCA TAC CTT GTA Met Leu Ser Gln Thr Lys Gln Gly Glu Asn Phe Pro Tyr Leu Val 290 295 300	912
GCG TAC CAA GCA ACA GTC TGT GTT CGC GCG AAA GCG CCC CCC CCC AGC Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro Pro Pro Ser 305 310 315 320	960
TGG GAC ACA ATG TGG AAA TGC ATG CTC CGT CTC AAA CCG ACT TTA ACT Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro Thr Leu Thr 325 330 335	1008
GGC CCT ACT CCC CTC TTG TAC AGG CTG GGG CCC GTC CAG AAT GAG ATC Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile 340 345 350	1056
ACA CTG ACG CAC CCC ATC ACC AAG TAC ATT ATG GCT TGC ATG TCT GCG Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala 355 360 365	1104
GAC TTG GAG GTC ATT ACC AGC ACT TGG GTT CTG GTG GGG GGC GTT GTG Asp Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly Gly Val Val 370 375 380	1152
GCG GCC CTG GCG GCC TAC TGC TTG ACG GTG GGT TCG GTA GCC ATA GTC Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val Ala Ile Val 385 390 395 400	1200
GGT AGG ATC ATC CTC TCT GGG AAA CCT GCC ATC ATT CCC GAT AGG GAG Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu 405 410 415	1248
GCA TTA TAC CAG CAA TTT GAT GAG ATG GAG GAG TGC TCG GCC TCG TTG Ala Leu Tyr Gln Phe Asp Glu Met Glu Glu Cys Ser Ala Ser Leu 420 425 430	1296
CCC TAT ATG GAC GAG ACA CGT GCC ATT GCC GGA CAA TTC AAA GAG AAA Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe Lys Glu Lys 435 440 445	1344
GTG CTC GGC TTC ATC AGC ACG ACC GGC CAG AAG GCT GAA ACT CTG AAG Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu Thr Leu Lys 450 455 460	1392
CCG GCA GCC ACG TCT GTG TGG AAC AAG GCT GAG CAG TTC TGG GCC ACA Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe Trp Ala Thr 465 470 475 480	1440

TAC
Tyr

1443

(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

```

Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe
 1             5             10             15

Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val Ile Ile Cys
      20             25             30

Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr
      35             40             45

Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala
      50             55             60

Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn Ile Glu
      65             70             75             80
Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Gly Arg Ala
      85             90             95

Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His
      100            105            110

Ser Lys Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr Ser Leu Gly
      115            120            125

Val Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ala Val Ile Pro
      130            135            140

Thr Ala Gly Asp Val Val Val Cys Ser Thr Asp Ala Leu Met Thr Gly
      145            150            155            160

Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser Ala Val Thr
      165            170            175

Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr
      180            185            190

Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr
      195            200            205

Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala Gly Glu Arg
      210            215            220

Pro Ser Asp Met Phe Asp Ser Val Val Leu Cys Glu Cys Tyr Asp Ala

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225	230	235	240
Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr Val Arg Leu	245	250	255
Arg Ala Tyr Ile Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu	260	265	270
Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile Asp Ala His	275	280	285
Met Leu Ser Gln Thr Lys Gln Gly Gly Glu Asn Phe Pro Tyr Leu Val	290	295	300
Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro Pro Pro Ser	305	310	315
Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro Thr Leu Thr	325	330	335
Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile	340	345	350
Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala	355	360	365
Asp Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly Gly Val Val	370	375	380
Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val Ala Ile Val	385	390	395
Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu	405	410	415
Ala Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser Ala Ser Leu	420	425	430
Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe Lys Glu Lys	435	440	445
Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu Thr Leu Lys	450	455	460
Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe Trp Ala Thr	465	470	475
480			
Tyr			

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Figure 1

HCV-1	7932	CTCCACAGTCACTGAGAGCGACATCCGTACGGAGGAGGCAATCTACCAAT	7981
HCV-J	1a	---A-G---	---A-T---
BE90	1b	---A-----C-----A-----	---A-----T-----
2TY4	1c	---A-----C-----A-----	---A-----T-----
4TY4	1c	---A-----C-----A-----	---A-----T-----
HC-J6	2a	---A-C-----A-----A-G-T-----T-C-A-A-T-GGG	---A-T-----T-C-A-A-T-GGG
HC-J8	2b	---A-C-----G-----G-----AA-A-A-A-A-AT-C-A-T-GG	---A-T-----T-C-A-A-T-GG
NE91	2b	---A-C-----G-----G-----T-AA-A-A-A-AT-C-A-T-G	---A-T-----T-C-A-A-T-G
EB12	2b	---A-C-----G-----G-----T-AA-A-A-A-AT-C-A-T-G	---A-T-----T-C-A-A-T-G
ARG6	2c	---A-C-----G-----G-----T-AA-A-A-A-AT-C-A-T-G	---A-T-----T-C-A-A-T-G
ARG8	2c	---A-C-----G-----G-----T-AA-A-A-A-AT-C-A-T-G	---A-T-----T-C-A-A-T-G
I10	2c	---A-C-----G-----G-----T-AA-A-A-A-AT-C-A-T-G	---A-T-----T-C-A-A-T-G
T983	2c	---A-C-----G-----G-----T-AA-A-A-A-AT-C-A-T-G	---A-T-----T-C-A-A-T-G
NE92	2d	---A-G-----G-----G-----A-A-T-----T-C-A-A-TTG	---A-T-----T-C-A-A-TTG
CHR20	3a	---T-T-----ACAG-----A-GGT-----A-----AG-A-----G	---A-T-----T-C-A-A-TTG
CHR21	3a	---G-T-----ACAG-----A-GGT-----A-----AG-A-----G	---A-T-----T-C-A-A-TTG
CHR22	3a	---A-T-----ACAG-----A-GGT-----A-----AG-A-----G	---A-T-----T-C-A-A-TTG
T1	3a	---A-T-----ACAG-----A-GGT-----A-----AG-A-----G	---A-T-----T-C-A-A-TTG
T7	3a	---A-T-----ACAG-----A-GGT-----A-----AG-A-----G	---A-T-----T-C-A-A-TTG
NE93	3a	---G-T-----ACAG-----A-GGT-----A-----AG-A-----G	---A-T-----T-C-A-A-TTG
NZL13	3a	---A-T-----ACAG-----A-GGT-----A-----AG-A-----G	---A-T-----T-C-A-A-TTG
EB1	3a	---A-T-----ACAG-----A-GGT-----A-----AG-A-----G	---A-T-----T-C-A-A-TTG
EB2	3a	---A-T-----ACAG-----A-GGT-----A-----AG-A-----G	---A-T-----T-C-A-A-TTG
EB3	3a	---A-T-----ACAG-----A-GGT-----A-----AG-A-----G	---A-T-----T-C-A-A-TTG
EB7	3a	---A-T-----ACAG-----A-GGT-----A-----AG-A-----G	---A-T-----T-C-A-A-TTG
T9	3b	---T-T-----ACAT-----A-G-----A-G-----AG-A-----	---A-T-----T-C-A-A-TTG
T10	3b	---T-T-----ACAG-----A-G-----A-G-----AG-A-----	---A-T-----T-C-A-A-TTG
BE98	3c	---T-T-----ACAG-----A-G-----A-G-----AG-A-----	---A-T-----T-C-A-A-TTG

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Figure 1 - Continued 1

GB48	4c	7932	7981
GB116	4c	---T-A-C-A-AG---	AGG---T-G-
GB215	4c	---T-A-C-A-AG---	AGG-A-T-G-
GB358	4c	---T-A-C-A-AA---	AGG-A-T-G-
GB809	4e	---T-A-C-A-AG---	AGG-G-T-G-
CAM600	4e	---T-G---A---	---A-A-G-T-G-
CAMG22	4f	---T-G---A---	---A-A-G-T-G-
GB549	4g	---G-G-C-A-A---	---A-AGG---G-
GB438	4h	---G-G-C-A-G-T---	---A-AG---G-
CAR4/1205	4i	---G-G---A-G---	---A-AG---G-
CAR1/501	4j	---C-G-N---G-N---	---A-AGG-T-G-
EG-13	4k	---G-T-GN-C---G---	---GA-AGG-T-G-
EG-19	4k	---	---G---T-G-
BE95	5a	---G-C-T-C-ACAT---	---AATG-C-A-T-C-T---
BE96	5a	---A-C-C---C-ACAT---	---AATG-T-A-T-C-A---
CHR18	5a	---G-C-T-C-ACAT---	---AATG-T-A-T-T-T---
CHR19	5a	---G-C-T-C-ACAT---	---AATG-T-A-T-C-T---

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Figure 1 - Continued 2

	SEQ ID	7982	8031
HCV-1	1a	GTGTGACCTCGACCCCAAGCCCGGTGGCCATCAAGTCCCTCACCGAG	
HCV-J	1b	-----T-G-C-----G-G-----A-GCA-----A-G-----G-----A-----	
BE90	1b	-----T-G-C-----G-G-----A-ACA-----A-----G-----A-----	
2TY4	1c	-----GC-----G-C-A-----T-----AAAT-----T-----	
4TY4	1c	-----GC-----G-C-A-----CT-----AAAT-----T-----	
HC-J6	2a	C-----TC-T-GCC-GAGG-G-----A-ACT-----AC-C-A-G-T-----	
HC-J8	2b	C-----TCT-GCCT-AAG-----A-AACT-T-----AC-C-G-----T-----	
NE91	2b	C-----TC-----GCC-AAG-G-----A-AACT-T-----AC-C-G-----	
EB12	2b	C-----TC-----GCCT-AAG-G-----A-AACT-T-----AC-C-G-----T-----	
ARG6	2c	CC-----TCA-GCCTGAGG-G-----T-AACT-----AC-C-A-G-T-----	
ARG8	2c	CC-----TCA-GCC-GAGG-G-----T-AACT-----AC-C-A-G-T-----	
I10	2c	CC-----CTCA-GCCTGAGG-G-----AACT-----T-AC-C-A-G-T-----	
T983	2c	C-----TCA-GCCT-AGG-G-----T-GACT-----T-AC-C-AT-G-T-----	
NE92	2d	C-----CTCTT-ACC-GAG-G-----A-GACT-----AC-C-A-G-T-----	
CHR20	3a	C-----C-A-----T-A-GG-G-----A-GAAA-TG-----TCC-----G-----	
CHR21	3a	C-----C-A-----T-A-GG-G-----A-GAAA-TG-----TCC-----G-----	
CHR22	3a	C-----C-A-----T-A-GG-G-----A-GAAA-TG-----TCC-----G-A-----	
T1	3a	C-----C-A-----T-A-GG-G-----A-GAGA-TG-----TCC-----G-----	
T7	3a	-----A-T-----T-G-GG-G-----A-GAAA-TG-----TCC-----G-----	
NE93	3a	C-----CA-----T-A-GG-G-----A-GAAA-TG-----TCC-----G-----	
NZL13	3a	C-----C-A-----T-A-GG-G-----A-GAAA-TG-----TCC-----G-----	
EB1	3a	C-----C-A-----T-A-GG-G-----A-GAAA-TG-----TCC-----G-----	
EB2	3a	C-----C-A-----T-A-GG-G-----A-GAAA-TG-----TCC-----G-A-----	
EB3	3a	C-----C-A-----T-A-GG-G-----A-GAAA-TG-----TCC-----G-----	
EB7	3a	C-----C-A-----T-A-GG-G-----A-GAA-TG-----TCC-----G-----	
BR33	3a	9,11	-----G-----
BR34	3a	1,3	-----G-A-----
BR36	3a	5,7	-----G-----
T9	3b		-C-----T-G-AG-G-T-GAA-----G-----GCG-T-----A-----

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Figure 1 - Continued 3

	SEQ ID	7982	8031
T10	3b	-C-----T-G--AG-G--T-GAA--G---GCG-T---A---	
BE98	3c	CC-----A-GGA-G-G-TA-GAG-TG-A-CT--A---G---	
GB48	4c	-----G-G--G-----AA--A--T-CCG---A-A---	
GB116	4c	-----G-G--G-----AGA--A--T-CCG---A-A---	
GB215	4c	-----G-G--G-----AA-TA--T-CCG---A-A---	
GB358	4c	-----G-G--G-G-----AA--A--T-CTG---A-A---	
GB809	4e	-----G-G--G-G-----AA-TA-AGCG---G---	
CAM600	4e	-----T-G-G--G-G-----AA-TA--A-CCG---G---	
CAMG22	4f	-----G-G--TG-A-----AA-TA-ATCTG---T-A---	
GB549	4g	-C-C-----G-G--G-----AA-TG-ATCCG--A-G-A---	
GB438	4h	-C-----G-G--G-G-A---AA-TG-ATCCG-T---A-A---	
CAR4/1205	4i	-C--A-T-G-GN-G-T-N---AA-T---CG---A---	
CAR1/501	4j	---C-----G-A-GG-----AA-TA---CCG---T---	
EG-13	4k	---A-----G-G--G-----T-AA--T--T-CTG---A-A---	
EG-19	4k	---AGT--G-G-T-G-G-T---AA-TT--T-CTG---G-A---	
BE95	5a	CA-----T-GC-G--G-G-A---CA-A-ACG--A---C-A---	
BE96	5a	CA-----TCGC-G--G-C-A---CA-A-ACG--A---C-A---	
CHR18	5a	CA-TGT--T-GC-G--TG-G-G-T---A-ACG--A---C-A---	
CHR19	5a	CA-TGT--T-GC-G--TG-G-A---C--A-ACG--A---C-A---	

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Figure 1 - Continued 4

		8032	8081
		AGGCTTTATGTTGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTGCGG	
HCV-1	1a	C-----C-----T-C-G-T-----G-A--C-----T-----	
HCV-J	1b	C-----A-C-----T-C-G-T-----A--C-----T-----	
BE90	1b	--AT-G-C-C-A-G-C-G-----A--T-A-----	
2TY4	1c	--AT-G-C-C-T-G-CT-G-T-----AA-C-----	
4TY4	1c	--A--C-G-A-G-CA-GTT--CAGC-A--CC-C-----	
HC-J6	2a	--A--C-C-A-A-G-CA-G-A--CAGC-AA--C-ATC-----	
HC-J8	2b	--A--C-C-G-A-G-CA-G-TA--CAGC-AA--C-ATC-----	
NE91	2b	--A--C-C-A-A-G-CA-G-A--CAGC-AA--C-ATC-----	
EB12	2b	--G-C-C-A--G-CA-G-A--CAGC-AA--C-ATC-----	
ARG6	2c	--A-A-C-A--G-CA-G-A--CAGC-A--CC-ATC-----	
ARG8	2c	--A-G-C-A--G-CA-G-A--CAGC-A--C-ATC-----	
I10	2c	--A-A-C-G-A-G-CA-G-A--CAGC-AA--C-TC-----	
T983	2c	-----C-G-A-G-CA-GCTA--CAGC-AA--C-A-C-----	
NE92	2d	C-----CTGC-----A-GTT--CAGC-A--CCC-G-T-----	
CHR20	3a	C-----CTGC-----A-GTT--AGC-A--CCC-G-T-----	
CHR21	3a	C-----CTGC-----A-GTT--CAGC-A--CCC-G-T-----	
CHR22	3a	C-----CTGC-----A-GTT--CAGC-A--CCC-A-T-----	
T1	3a	C-----CTGC-A-----A-GTA--CAGC-A--TCC-G-T-----	
T7	3a	C-----CTGC-A-----A-GTTT--CAGC-A--CCC-G-T-----	
NE93	3a	C-----CTGC-----A-GTT--CAGC-A--CCC-G-T-----	
NZL13	3a	C-----CTGC-----CA-GTT--CAGC-A--CCC-G-T-----	
EB1	3a	C-----CTGC-----CA-GTT--CAGC-AA--CCC-G-T-----	
EB2	3a	C-----CTGC-----A-GTT--CAGC-AA--CCC-G-T-----	
EB3	3a	C-----CTGC-----A-GTT--CAGC-AA--CCC-G-T-----	
EB7	3a	C-----CTGC-----A-GTT--CAGC-A--CCC-G-T-----	
BR33	3a	C-----CTGC-----A-GTT--CAGC-A--CCC-G-T-----	
BR34	3a	C-----CTGC-----A-GTT--CAGC-A--CCC-G-T-----	
BR36	3a	C-----CTGC-----A-GTTT--CAGC-AA--CCC-G-T-----	
T9	3b	C-----G--CA-C-A--T--CA-GTA--CAGT-A--CTCC-G-----	

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Figure 1 - Continued 5

T10	3b	C-----G--CA-C-A-T--CA-GTA--CAGT-A--CTCC-G----
BE98	3c	C-----CTG--T-T--A-GTT--CAGC-A--AC-AC-----
GB48	4c	--A-C-C-C-G-C-T--CA-GCAT--CAGC-A--A--CCTG----
GB116	4c	--A-C-C-C-G-C-T--CA-GCAT--CAGC-----A--CCTG----
GB215	4c	--A-C-----G-C-T--CA-GCAT--AGC-AA--A--CCTG----
GB358	4c	--A-C-----G-C-T--CA-GCAT--CAGC-A--A--CCTG-T--
GB809	4e	--A-C-C-C-G-C-----CA-GCAT--CAGC-A--A--CCTT-T--
CAM600	4e	--A-C-C-C-G-C-----A-GTA--AGC-A--A--CCTT-----
CAMG22	4f	--A-C-----G-C-T--CA-GCA--CAGC-----A--CCTA----
GB549	4g	--A-C-C-C-G-C-T--CA-GTA--C-C-A-----CCTA-----
GB438	4h	--A-C-C-CAAG-C-----CA-GTAT--CAGC-A-----CCTA----
CAR4/1205	4i	--A-C-C-G-C-----A-GCA--CAGC-A--A--CCTG-T--
CAR1/501	4j	--A-C-----G-C-A--CA-GTT--CAGC-A--A--CCTG-T--
EG-13	4k	--A-C-C-C-G-C-----CA-GCA--CAGC-A--A--CCTT-T--
EG-19	4k	--A-C-C-C-G-C-----CA-GCA--AGC-A--A--CCTT-T--
BE95	5a	C-C-C-CTG-A-----CA-GTA--CAGC-A--C-AC-G-T--
BE96	5a	C-CT-G-TCUG-A-----CA-GTAT--CAGC-A--C-AC-A-T--
CHR18	5a	C-C-G-CTG--A-----CA-GTAT--CAGC-A--C-AC-A-T--
CHR19	5a	C-C-G-CTG--A-----CA-GTAT--CAGC-A--C-AC-A-T--

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Figure 1 - Continued 6

		8082				8131
HCV-1	1a	CTATCGCAGGTCCGCGCGAGCGGCTACTGACAACTAGCTGTGGTAACA				
HCV-J	1b	T-----C-----A-T-----G-----G-----C-C-----				
BE90	1b	-----C-A-----A-----G-----G-C-----C-----T-----				
2TY4	1c	-----T-----C-----C-----C-----C-----C-----				
4TY4	1c	-----T-----C-----C-----C-----C-----C-----				
HC-J6	2a	G-CA-GC-T-----C-----G-G-T-T-C-----ATG-G-----				
HC-J8	2b	-----CA-GC-T-----A-----T-TT-C-C-C-----ATG-G-T-----				
NE91	2b	T-CA-GC-T-----A-----T-TT-C-C-C-----ATG-G-T-----				
EB12	2b	T-CA-GC-C-----A-----T-TT-C-T-C-----ATG-G-T-----				
ARG6	2c	G-CA-GC-T-----ARG-G-----A-G-C-C-C-----ATG-----				
ARG8	2c	G-CA-GC-T-----CA-GC-T-----CA-G-C-C-C-----ATG-C-----				
I10	2c	G-CA-GC-T-----I10-A-----A-G-C-C-C-----ATG-C-----				
T983	2c	T-CA-GC-T-----T-----TG-G-C-C-C-----ATG-----				
NE92	2d	A-CA-AC-C-----C-----A-GT-C-C-----ATG-A-T-----				
CHR20	3a	T-----C-T-----T-T-T-A-C-C-T-C-----TC-C-----				
CHR21	3a	T-----C-T-----T-T-T-A-T-C-T-C-----TC-C-----				
CHR22	3a	T-----C-T-----T-T-T-A-T-C-T-C-----TC-C-----				
T1	3a	T-----C-----T-C-T-A-C-C-T-C-----TC-C-----				
T7	3a	T-----C-C-----T-C-T-A-C-C-T-C-----TC-C-----				
NE93	3a	T-----C-T-----T-C-T-A-T-C-T-C-----T-----				
NZL13	3a	T-----C-T-----T-C-T-A-T-C-T-C-----TC-C-----				
EB1	3a	T-----C-T-----T-C-T-A-T-C-T-C-----TC-C-----				
EB2	3a	T-----C-T-----T-C-T-A-T-C-T-C-----TC-C-----				
EB3	3a	T-----C-T-----T-C-T-A-T-C-T-C-----TC-C-----				
EB7	3a	T-----C-T-----T-C-T-A-T-C-T-C-----TC-C-----				
BR33	3a	T-----C-T-----T-C-T-A-T-C-T-C-----T-TC-C-----				
BR34	3a	T-----C-C-----T-C-T-A-T-C-T-C-----TC-C-----				
BR36	3a	T-----C-T-----T-C-T-A-T-C-T-C-----TC-C-----				
T9	3b	-----C-C-----C-----CT-C-T-C-----TC-C-T-----				

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Figure 1 - Continued 7

T10	8082	3b	8131
BE98		3c	
			-----C-C-----C-----CT--C-T-C-----TC-C-T-
			T-C-C-C-----T-T-T-G-G-AC-C-C-----TC-G----
GB48		4c	G-----A-T-----A-----CTAC-C-C-----TC-G----
GB116		4c	G-----A-----T-----CTAC-C-C-----TC-G----
GB215		4c	G-----A-----A-----CTAC-C-C-----TC-G----
GB358		4c	G-----A-----A-----CTAC-C-C-----TC-G----
GB809		4e	G-----T-A-----A-----TAC-C-C-----TC-G----
CAM600		4e	G-----A-----A-----TAT-C-C-----TC-G----
CAMG22		4f	G-C-T-A-----A-----TAC-C-A-----TC-G----
GB549		4g	GC-A-G-----A-----G-CTAC-C-C-----TC-G----
GB438		4h	GCT-G-----A-----G--TAC-C-A-----TC-G----
CAR4/1205		4i	-ATC-T-A-----A-----TTAC-C-G-----TC-A----
CAR1/501		4j	AC-A-C-----A-----GT-C-C-C-----TC-G----
EG-13		4k	G-----G-A-T-G-A-----A-CT-T-G-C-----TC-A----
EG-19		4k	G-C-G-A-----G-A-----A-CTAT-G-C-----TC-A----
BE95		5a	T-----A-----C-----TT-C-C-C-----TATG-C----
BE96		5a	T-----A-----C-----CT-C-C-C-----TATG-C----
CHR18		5a	T-----T-A-----C-----CT-C-C-C-----TATG-C----
CHR19		5a	T-C-T-A-----C-----CT-C-C-C-----TATG-C----

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Figure 1 - Continued 8

		8132			8181
HCV-1	1a	CCCTCACATTGCTACATCAAGCCCGGCGAGCCTGTCGAGCGCAGGGGCTC			
HCV-J	1b	-----A-T---T-G-----ACT-G-----T---AA-----			
BE90	1b	-----T-A-T---C-A-----TCT-----T-GAA-----			
2TY4	1c	-----C-----TA-----			
4TY4	1c	-----C-----TA-----			
HC-J6	2a	-----A---A---TG-G-A---TTA-G-----AAG-T---A-A			
HC-J8	2b	-----A-G-A-T-----A---TT---G---AAG-T---A-A			
NE91	2b	-----A-G-G-T-----A---TT---G---AA-----A-			
EB12	2b	-----A-G-A-----A---TT---G---CAA-T-G---A-			
ARG6	2c	-----A---G---G-G-A-TAAA-G-A---AAC---G-CA-T			
ARG8	2c	-----A---G---G-G-A-A---G-G---AAC---G-CA-T			
I10	2c	-----G---G---G-G-A-A-A-G-G---AAC---G-CA-T			
T983	2c	-----A-T-G-T---G-G-A-AA---G---CAAC---TG-CA-T			
NE92	2d	-----A---G---G-G---A-AA---AAG-T-G-CA-A			
CHR20	3a	-----AA---T---T---TA-A-G---T-CGAAG---C---			
CHR21	3a	-----AA---T---T---TA-A-G---TGCGAAG---C---			
CHR22	3a	-----AA---T---T---A-TA-A-G---TGCCGA---C---			
T1	3a	-----AA---T---T---ACA-G---TGCGAAG---C---			
T7	3a	-----GA---T---T---ACA-G---TGCAA-G---C---			
NE93	3a	-----AA---T---T---ACAA-G---GCGAAG---C---			
NZL13	3a	-----AA---T---T---ACA-G---TGC-AAG---AAC---			
EB1	3a	-----AA---T---T---A-TACA-G---CGAG---C---			
EB2	3a	-----AA---T---T---ACA-G---CGAG---C---			
EB3	3a	-----AA---T---T---ACA-G---CAAG---C---			
EB7	3a	-----AA---T---T---ACA-G---CAA---C---			
BR33	3a	-----AA---T---T---ACA-G---TGCAA---C---			
BR34	3a	-----AA---T---T---ACA-G---TGCAA-G---C---			
BR36	3a	-----AA---T---T---A-ACA-G---GCAA---C---			
T9	3b	-----AA-A-C-T-----ACT-----A-CA-G-T-G-T			

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Figure 1 - Continued 9

T10	8132	-AA-A-C-T-----	ACT--G--A-CA-G-T-G-T--	8181
BE98	3b	-AA--C-T-----	-A-AAA-----TACCAA--T-C-AA-T	
	3c			
GB48	4c	-A-G-G-----C--A--TCA-C-TATCAA--G-G-----G		
GB116	4c	-A-G-G-----TC--A--TCA-C-TATCA--G-G-----G		
GB215	4c	-A-G-G-----TC--A--TCA-C-ATCA-G-GT-----G		
GB358	4c	-A-G-G-----C--A--TCA-C-TATCA--G-G-----G		
GB809	4e	-AA-G-G-----C-T--TCA--ATCA-G-T-G-----A		
CAM600	4e	-A-G-G-----C-T-A--TCA--ATCA-G-T-G-----G		
G22	4f	-T-G-G-----T-C--ACA-G--ACCAA--T-C-A--		
GB549	4g	-TG-A-G-T-TC--GTT-G-TAC-A-G--T--G		
GB438	4h	-GG-G-A-----C-T-A--ACA--ACCA-G-T-----G		
CAR4/1205	4i	-G-G-----C--A--ACA-G--ACCA-G--G-CT-G		
CAR1/501	4j	-A-G-G-----C-T-A--ACA-T-TAC-A--A-C-CT-A		
EG-13	4k	-G-G-G-----C-A-A--AC-C-TAT-A--G-G-----G		
EG-19	4k	-G-G-G-----C--A--ACA-C-TAT-A-G-G-A-A		
BE95	5a	-A-G-G-----TTTA-CT--A--A--		
BE96	5a	-A-G-G-----T--TTTA-CT--A-A--T--		
CHR18	5a	-A-G-G-----T--TTTA-CT--A--T--		
CHR19	5a	-A-G-G-----TTCA-C--A--T-AA--		

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Figure 1 - Continued 10

		8182	8231
HCV-1	1a	CAGGACTGCACCATGCTCGTGTGTGGCAGACTTAGTCTGTATCTGTGA	
HCV-J	1b	-----G-----AAC-A-----C-T-----	
BE90	1b	-----G-----C-G-----C-T-----	
2TY4	1c	-G-----	
4TY4	1c	-----	
HC-J6	2a	ATT-CGCC--A-----G-A-C-----T-----G-T-C-----CA--	
HC-J8	2b	GT--CCTGTT--T-G-----A-----C-G-----C-----CA--	
NE91	2b	GT--CC-GT--G-----A-----C-G-----C-----CG--	
EB12	2b	GT-----CC-GTT--	
ARG6	2c	GTT-C-CC----	
ARG8	2c	GTT-CTCC----	
I10	2c	GTT-CTCC----	
T983	2c	GTT-CT-C----	
NE92	2d	ATT-C-CC--G-----G-----C-----TC-----T-C-----CA--	
CHR20	3a	-G-A--CCGGA-T-T--T-C-C-A-T--TC-G-----GG-GGC--	
CHR21	3a	-G-AC-CCGGA-T-T--C-C-A-T--TC-G-T--GG-GGC--	
CHR22	3a	-G-A--CCGGA-T-T--T-C-C-A-T--TC-G-T--GG-GGC--	
T1	3a	-G-A--CCGGA-T-T--T-C-C-A-T--TC-G-----AG-GGC--	
NE93	3a	-G-A--CCGGA-T-T--T-C-C-A-T--TC-G-----GG-GGC--	
NZL13	3a	-G-A--CCGGA-T-T--T-C-C-A-T--TC-G-----GG-GGC--	
EB1	3a	-G-A--CCGGA--	
EB2	3a	-G-A--CCGGA--	
EB3	3a	-G-A--CCGGA--	
EB7	3a	-G-A--CCGGA--	
BR33	3a	-G-A--CCGGA-T-T--T-T-C-A-T--T-G-----GG-GGC--	
BR34	3a	-G-A--CCGGA-T-T--T-T-C-A-T--TC-G-----GG-GGC--	
BR36	3a	-G-AG-CCGGA-T-T--T-T-C-A-T--TC-G-----GG-GGC--	
T9	3b	A-A--CCCAT-TT-C-T-T-C-C-A-T--T-G-G-A-C-----	

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Figure 1 - Continued 11

		8182			8231
T10	3b	A-A--CCAT--T-C-T-C-C-C-A--T-T-G-G--G-G-C--			
BE98	3c	A-AA-TCCAT-AT-C-T-C-C-C-A-T--G--G--TGC--			
GB48	4c	AGA-----T-G-C-----T-T-C-G-T-C--GC--			
GB116	4c	AGA-----T-G-C-----T-T-C-G--C-TGC--			
GB215	4c	AGA-----T--G-C-A--T--C-G--C-TGCC--			
GB358	4c	AGA-----T-G-C-----T-T-C-G--C-GC--			
GB809	4e	A--T-----G-T-C-T--C--G-GCC--			
GB809	4e	A-----G-T-C-T--C--G-GC--			
CAM600	4e	A-----T-G-T--T--G-GC--			
G22	4f	A--T-----T-G-T--T--G-GC--			
GB549	4g	A-A-GT---G--G-T--A-----C--			
GB438	4h	A-A-T---T--G-A-C-T--T--TGCC--			
CAR4/1205	4i	A--T-----G-C-C-N--C-G-T-C-TGC--			
CAR1/501	4j	A-A-T-----G-C-C-T--T--T-CC--			
EG-13	4k	AGA-----T			
EG-19	4k	A-A--A---T			
BE95	5a	-G-----GC-C-G-----T--TC-T-G-CC--C--			
BE96	5a	-G-----A--GC-C-G-----T--TCAT-G-CC--C--			
CHR18	5a	-----GC-C-G-----T--T-TC-T-G-CC-T-C--			
CHR19	5a	-----GC-C-G-----T--TTAC--G-G-CC-T-C--			

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Figure 1 - Continued 12

		8232		8271
HCV-1	1a	AACGCGGGGTCCAGGAGGACGCGCGAGCCTGAGAGCC		
HCV-J	1b	G--T---AAC--	T---GC--AC---	
BE90	1b	---AAC--A---	---AC---	
HC-J6	2a	G--CA---AC-G---	A-CG-A---	
HC-J8	2b	G--CAA-TAA-G---	A-CGA-A---	T
NE91	2b	G--CA---TAA-G---	A-CGA-A---	T
NE92	2d	G--TCA---AC-G---	A-CG-A---	AC---
CHR20	3a	G--T-AT-C--G-C---	TAGA--AGC---	
CHR21	3a	G--T-AT-C--G-C---	TAGAA--AGC--C---	
CHR22	3a	G--T-AT-C--A-T---	TAGA--AGC--G---	
T1	3a	G--AT-C--G-T---	TAGA--AGC---	
T7	3a	G--T-AT-C--G-C---	TAG-A--GC---	
NE93	3a	G--T-AT-C--G-C---	TAGA--AGC---	
NZL13	3a	G--T-AT-C--G-T---	TAGA--AGC---	
BR33	3a	G--T		
BR34	3a	G--T		
BR36	3a	G--T		
T9	3b	---	TGC-C--G-----AGA--AGCT--C-----	
T10	3b	---	TGC-C--G-----AGA--AGCT--C-----	
BE98	3c	---	G--T-A--A--G-T-----AGA---	

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Figure 1 - Continued 13

GB48	4C	8232	G----	AT--C-AG-----	AAACGACC-----	CG----	8271
GB116	4C		----	AT-C-AG-----	AAACGAGC-----	CG----	
GB215	4C		G----	AT-C-AG-----	AAACGAGC-----	CG--T-	
GB358	4C		G----	AT-C-TG-----	AAACGAGC-----	CG----	
GB809	4e		G----	GT-C-TG-----	AA-CGAGC-----	CG--T	
CAM600	4e		----	GT-C-G-----	AA-CGAGC-----	CG--T	
G22	4f		----	AT-T-G-A-----	CGCCGAGC-----	CG--T	
GB549	4g		G----	GC-C-AG-----	T-AAAGGC-----	CC----	
GB438	4h		----	GT-C-GG-----	CCGAGC-----	CC----	
CAR4/1205	4i		G----	ATT-CA-AG-C-----	AA-CAAGC-----	CC-NA-T	
CAR1/501	4j		G----	C-T-GG-----	TC-CANA-C-----	NNC-C-N	
BE95	5a		G--CA--	ACA-C-----	T-AA-A-----	A-----	
BE96	5a		G--CA--	ACA-C-----	T-AA-A-----	A-----	
CHR18	5a		G--CA--	ACG-C-----	TAAA-----	-----	
CHR19	5a		G--CAA-	ACG-C-----	T-AA-----	T-----	

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Figure 2

	SEQ ID	2645	2694
1a		STVTESDIRTEEAIVQCCLDPQARVAIKSLTERLYVGGPLTNSRGECG	
1b		-----N-----S-----A-E-Q-R-----K-Q-----	
1c	214	-----N-----V-S-----A-E-Q-----I-----K-Q-----	
1c		-----H-D-----N-----K-----	
1c		-----H-D-A-N-----K-----	
2a		-----R-----S-RA-S-PEE-HT-H-----MF-K-QT-----	
2b		-----R-----S-A-S-POE-TV-H-----M-K-QS-----	
2b	216	-----R-----S-A-S-POE-TV-H-----MI-K-QS-----	
2b		-----A-S-POE-TV-H-----M-K-QS-----	
2c		-----S-S-PEE-T-H-----M-K-QS-----	
2c		-----LS-S-PEE-T-H-----M-K-QS-----	
2c		-----A-S-POE-T-H-----M-K-QS-----	
2c	T983	-----A-S-POE-T-H-----M-K-QS-----	
2d	146	-----R-----S-LA-S-PB-T-H-----ML-K-QT-----	
3a		-----Q-V-E-----N-E-E-KV-S-----C-MF-K-AQ-----	
3a		-----Q-V-E-----N-E-E-KV-S-----C-MF-K-AQ-----	
3a		-----Q-V-E-----N-E-E-KV-S-----C-MF-K-AQ-----	
3a		-----Q-V-E-----N-E-E-KV-S-----C-MF-K-AQ-----	
3a	218	-----Q-V-E-----N-E-E-KV-S-----C-MY-K-VQ-----	
3a		-----Q-V-E-----N-E-E-KV-S-----C-MF-K-AQ-----	
3a		-----Q-V-E-----N-E-E-KV-S-----C-MF-K-AQ-----	
3a		-----N-E-E-KV-S-----C-MF-K-AQ-----	
3a		-----N-E-E-KV-S-----C-MF-K-AQ-----	
3a		-----N-E-E-KV-S-----C-MF-K-AQ-----	
3a		-----N-E-E-KV-S-----C-MF-K-AQ-----	
3a	10, 12	-----N-E-E-KV-S-----C-MF-K-AQ-----	
3a	2, 4	-----N-E-E-KV-S-----C-MF-K-AQ-----	
3a	6, 8	-----N-E-E-KV-S-----C-MF-K-AQ-----	
3a		-----C-MF-K-AQ-----	
3a		-----C-MF-K-AQ-----	
3b		-----H-----E-----E-E-K-SA-----I-----MY-K-LQ-----	
3b		-----Q-----E-----E-E-K-SA-----I-----MY-K-LQ-----	
3b		-----A-----KDE-RV-T-----C-MF-K-QH-----	
3c	150		

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Figure 2 - Continued 1

EG13	4a	2645	V	N-E-E-K-TA	MH-K-DL	2694
EG19	4a		V	S-ELE-KV-TA	MH-K-DL	
GB48	4c		K-V-EV	E-E-K-TA	MH-K-DL	
GB116	4c	107	K-V-EV	E-E-R-TA	MH-K-DL	
GB215	4c	109	K-V-EV	E-E-KV-TA	MH-K-DL	
GB358	4c	111	K-V-EV	E-E-K-TA	MH-K-DL	
GB809	4e	113	R-KV-EV	E-E-KV-AA	MH-K-DL	
CAM600	4e	117	R-V-EV	E-E-KV-TA	MY-K-DL	
CAM622	4f	202	R-V-EV	E-E-KV-TA	MY-K-DL	
GB549	4g	204	R-V-EV	E-E-KV-TA	MY-K-DL	
GB438	4h	115	R-V-EV	E-E-KV-TA	MY-K-DL	
CAR4/1205	4i	208	R-V-EV	E-E-KV-TA	MY-K-DL	
CAR1/501	4j	210	P	R-X-V-EV	N-EXDX-KV-NA	MH-K-DL
		212	X-R	GEV	E-E-KV-TA	MF-K-DL
BE95	5a	160	H-M	S	S-Q-E-A-R-Q	C-MY-K-QQ
BE96	5a	162	A-H	L	S-SQ-D-A-R-Q	FC-MY-K-QQ
CHR18	5a		H-M	S	SLY-Q-E-R-Q	C-MY-K-QQ
CHR19	5a		H-M	S	SLY-Q-E-A-R-Q	C-MY-K-QQ

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Figure 2 - Continued 2

		2695	2744
HCV-1	1a	YRRCRASGVLTTSCGNTLCYIKARACRAAGLQDCTMLVCGDDLLVICE	
HCV-J	1b	-----L-T-----K-----N-----	
BE90	1b	-----L-S-----K-----	
2TY4	1c	-----L-----R-----	
4TY4	1c	-----L-----	
HC-J6	2a	-----M-I-V-L-K-IIAP-----S-	
HC-J8	2b	-----F-M-M-----L-K-IV-PV-----S-	
NE91	2b	-----F-M-M-----L-K-IV-PV-----S-	
EB12	2b	-----F-M-M-----L-K-IV-PV-----S-	
ARG8	2c	-----A-----M-----V-----N-IVAP-	
Il10	2c	-----M-----V-----N-IVAP-	
TR93	2c	-----V-----M-----V-K-N-IVAS-	
NE92	2d	-----F-M-I-V-Q-K-IIAP-----S-	
CHR20	3a	-----P-F-I-----SK-RNPDF-----VA-	
CHR21	3a	-----P-F-I-----AK-RTPDF-----VA-	
CHR22	3a	-----P-F-I-----AE-RNPDF-----VA-	
T1	3a	-----P-F-I-----T-AK-RNPDF-----VA-	
T7	3a	-----P-F-I-----T-A-RNPDF-----VA-	
NE93	3a	-----P-F-I-----TT-AK-RNPDF-----VA-	
N2L13	3a	-----P-F-I-----T-AK-N-RNPDF-----VA-	
EB1	3a	-----P-F-I-----T-B-RNPDF-----VA-	
EB2	3a	-----P-F-I-----T-E-RNPDF-----VA-	
EB3	3a	-----P-F-I-----T-K-RNPDF-----VA-	
EB7	3a	-----P-F-I-----T-K-RNPDF-----VA-	
BR33	3a	-----P-F-I-----T-AK-RNPDF-----VA-	
BR34	3a	-----P-F-I-----T-A-RNPDF-----VA-	
BR36	3a	-----P-F-I-----T-AK-RSPDF-----VA-	
T9	3b	-----P-F-I-----T-S-K-PSF-----VS-	
T10	3b	-----P-F-I-----T-S-K-PSF-----VS-	
BE98	3c	-----P-F-I-----K-TK-IKNPSF-----A-	

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Figure 2 - Continued 4

		2745	2757
HCV-1	1a	SAGVQEDAAASLRA	
HCV-J	1b	---T-----A---	
BE90	1b	---T-----V	
HC-J6	2a	-Q-TE--ERN---	
HC-J8	2b	-Q-NE--ERN---	
NE91	2b	-Q-NE--ERN---	
NE92	2d	-Q-TE--ERN---	
CHR20	3a	-D--D--R-A---	
CHR21	3a	-D--D--RTA---	
CHR22	3a	-D--N--R-A-G-	
T1	3a	-D--D--R-A---	
T7	3a	-D--D--RTA---	
NE93	3a	-D--D--R-A---	
NZL13	3a	-D--D--R-A---	
BR33	3a	-	
BR34	3a	-	
BR36	3a	-	
T9	3b	-C--E--R-A---	
T10	3b	-C--E--R-A---	
BE98	3c	---ID--R-	

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Figure 2 - Continued 5

GB48	4c	2745	2757
GB116	4c	-D--E--KRP-G-	
GB215	4c	-D--E--KRA-G-	
GB358	4c	-D--E--KRA-GV	
GB809	4e	-D--E--KRA-G-	
CAM600	4e	-G--E--KRA-G-	
G22	4f	-D--E--RRA-G-	
GB549	4g	-G--E--RA--	
GB438	4h	-G--E--RA--	
CAR4/1205	4i	-I-ID--KQA--T	
CAR1/501	4j	----E--PXTX-P	
BE95	5a	-Q-TH-E----	
BE96	5a	-Q-TH-E-N--	
CHR18	5a	-Q-TH-K----	
CHR19	5a	-Q-TH-E-C--V	

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Figure 3

	SEQ ID	
HCV-1	1	ATGAGCAGCAATCCTAAACCTCAAAAAAACAACAGTACACCAACCG
HCV-J	1a	-----A-----G-----C-----
HC-J6	1b	-----A-----G-----C-----A-A-----
HC-J8	2a	-----A-----G-----C-----A-A-----
HC-J8	2b	-----A-----G-----C-----A-A-----A-----
NE92	2d	-----A-----G-----C-----A-A-----T-----
EB1	3a	-----G-----C-----A-A-----T-----
NZL1	3a	-----ACT-----G-----C-----A-A-----T-----
HCV-TR	3b	-----ACT-----G-----C-----A-A-----ACT-----
BE98	3c	-----ACT-----A-----G-----C-----A-A-----S-----
GB358	4c	-----G-----C-----C-----
GB809	4e	-----T-----G-----C-----
CAM600	4e	-----G-----C-----
GB724	4?	-----G-----C-----
EG-29	4?	-----C-----
BE95	5a	-----G-----C-----A-A-----
51		
TCGCCACAGGACGTCAAGTTCCTCCGGGTGGCGGTACAGATCGTTGGTGGAG		
C-----T-----C-----T-----		
-A-----T-----C-----C-----C-----		
C-----T-----C-----T-----C-----		
C-----C-----T-----C-----		
-----A-----A-----		
-----A-----T-----C-----A-----		
C-G-----T-----A-----C-----		
C-----CAT-----T-----C-----T-----C-----		
C-----CAT-----T-----C-----		
C-----TAT-----A-----C-----T-----C-----		
C-----TAT-----A-----C-----T-----A-----C-----		
C-----CAT-----T-----T-----C-----C-----		
-----C-----T-----C-----		
5a		
HCV-1	1a	
HCV-J	1b	
HC-J6	2a	
HC-J8	2b	
NE92	2d	
EB1	3a	
NZL1	3a	
HCV-TR	3b	
BE98	3c	
GB358	4c	
GB809	4e	
CAM600	4e	
GB724	4?	
EG-29	4?	
BE95	5a	

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Figure 3 - Continued 1

101

HCV-1	1a	TTTACTTGTTCGCGCAGGGCCCTAGATTGGGTGCGCGCAGCAGAGA
HCV-J	1b	-----C-G-----T-G
HC-J6	2a	-A-----C-G-----A-G
HC-J8	2b	-C-----C-G-----A-G
NE92	2d	-A-----CC-G-----G
EB1	3a	-A-G-----AC-----C-T
NZL1	3a	-A-G-----AC-----C-T
HCV-TR	3b	-A-TG-C-----AC-----AGTAC-T
BE98	3c	-----G-C-A-A-----CCAG-----T-AGT-C-C
GB358	4c	-----C-G-----T-G
GB809	4e	-----G-----TC-G
CAM600	4e	-----C-G-----TC-G
GB724	4?	-----CC-G-----TC-G
EG-29	4?	-----GA-----TC-G
BE95	5a	-----GA-----TC-G

151

HCV-1	1a	AAGACTTCGAGCGGTGCGCAACTCGAGGTAGCAGTCAGCCTATCCCAA
HCV-J	1b	-----T-A-G-A-A-----
HC-J6	2a	-----G-----C-G-A-T-A-G-C-----C-----T-----
HC-J8	2b	-----T-----A-C-G-G-T-AC-----C-----C-----G-----
NE92	2d	-----A-----C-G-A-T-G-G-C-----C-----C-----
EB1	3a	-A-----T-A-----A-G-----C-AC-----A-----
NZL1	3a	-A-----T-A-----A-G-----C-AC-----A-----
HCV-TR	3b	-----G-----CAAACAG-----C-T-----
BE98	3c	-----CA-----G-C-A-C-----G-----
GB358	4c	-----G-----T-G-----
GB809	4e	-----G-----T-G-G-C-A-----
CAM600	4e	-----G-----T-G-G-C-A-----
GB724	4?	-----G-----T-C-G-----A-----
EG-29	4?	-----G-----T-G-----C-A-----A-----
BE95	5a	-----G-A-----C-T-AC-G-----T-----

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Figure 3 - Continued 2

201

HCV-1 1a GGCTCGTGGCCGAGGCGAGGACCTGGGTCAGCCCGGGTACCCCTTGGC
 HCV-J 1b C-----T-----
 HC-J6 2a -A-G-CT-ACT--AAT--GAA-A-A-A--C--
 HC-J8 2b A-A-G-CT-ACC--A-T--GAA-A-A-A--T--
 NE92 2d A-A-G-C-CT-CT--A-T--GAA-A-A-A--G--
 EB1 3a -G--AG--A--T--T-----G--
 NZL1 3a -G--AG--A--C-T-T-----G--
 HCV-TR 3b -CTC-G--C-T-----G--
 BE98 3c -G-C-AA--T-----G--
 GB358 4c -A--AT-T--A-T-----A--
 GB809 4e -G-C-AT--AT--G-----T--
 CAM600 4e -G-C-AA--AT--G-----T--
 GB724 4? -G-C-T--T--G-AG--C--
 EG-29 4? -G--AT--A-T--A-A-A-T-A--
 BE95 5a -G-C-A--AC--C-T--G--A--

251

HCV-1 1a CCTCTATGGCAATGAGGCTGCGGGTGGCGGGATGGCTCCTGTCTCCC
 HCV-J 1b C-----TATG-----A-----A--
 HC-J6 2a -A-C-G--ACT--C--A-----C--
 HC-J8 2b -G-C-A-C--T--C--T-----C--
 NE92 2d -G-C-G--CT--C--A-G--C--
 EB1 3a -T-C-----A-G--C-A--
 NZL1 3a -T-C--A--T--T--A--C-A--
 HCV-TR 3b -C-G-A--T--T--A--T--C--
 BE98 3c -A--G-----A-G--C-G--
 GB358 4c -T-T-C-T--T--T--A--G--
 GB809 4e -T-C-T--T--T--A-G--C-T--
 CAM600 4e -T-C-----T--A-G--C-T--
 GB724 4? -T-T-C-T-----A-G--T--
 EG-29 4? -T-T-C-T-----A-G--T--
 BE95 5a -T-C-C-----CT-----A-G--G--C--C--T--

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Figure 3 - Continued 3

	301	
HCV-1	1a	CGTGGCTCTCGGCTAGCTGGGGCCACAGACCCCGGCGTAGGTGCGG
HCV-J	1b	-----T-----
HC-J6	2a	--A-T-C-T-CTCT-----AT-----A-----C--
HC-J8	2b	--C-G-----T-----C-----A--A--A--
NE92	2d	--A-G-----C-GTCA-----A-T-----AC-----A--
EB1	3a	--C-----C-T-ATCT-----A-AT-----A-----C--
NZL1	3a	--C-----C-T-ATC-----A-AT-----G-----C--
HCV-TR	3b	-----T-----C-----T-----A-AT-----A-C--
BE98	3c	--C-----C-GTCG-----A-AT-----C--A
GB809	4e	--C-G-----GTCT-----T-AT-----G-----C--
CAM600	4e	--C-N-----N-GTCT-----AT-T-----N-G--A-C--
GB724	4?	--C-----ATCT-----A-AT-T-----G--A--
BE95	5a	--A-----AT-----AT-----A-AA-----
	351	
HCV-1	1a	CAATTGGGTAAAGTCATCGATACCCTTACGTGCGGCTTCGCCGACCTCA
HCV-J	1b	T-----A-----
HC-J6	2a	--CG-----A-----T-----
HC-J8	2b	-----C-GA-----A-----T-T-T-----
NE92	2d	--C-----T-----T-----T-----
EB1	3a	-----A-----C-----G--
NZL1	3a	-----A-----A-----A-----
HCV-TR	3b	--C-T-----A-----T-A-----
GB809	4e	--CC-----A--A-----
CAM600	4e	--C-----A--A-----
GB724	4?	-----C-----G-----
BE95	5a	T-----A-----A-----T-----

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Figure 3 - Continued 4

	401	
HCV-1	1a	CTGGGTACATACGGCTCGTGGCGCCCTCTTGGAGGCGGTGCCCAGGGCC
HCV-J	1b	-----T-----T-----C-A-G-----
HC-J6	2a	-----C-TG-----A-----G-C-C-----TC-----A-T
HC-J8	2b	-----C-TG-----T-----GG-----TC-----A-T
NE92	2d	-----C-TG-----AG-----T-T-TC-----A-T
NZL1	3a	-----C-----T-----G-A-----TC-A-A-----
HCV-TR	3b	-----T-----HCV-----G-G-G-----TC-A-A-----
GB809	4e	-----A-----C-----T-A-----CG-G-T-----TC-A-A-----
CAM600	4e	-----A-----C-----T-A-----CG-G-T-----TC-----
GB724	4?	-----A-----C-----G-----CG-C-G-----TC-----
BE95	5a	-----T-C-----A-G-CA-G-----TC-A-----T
	451	
HCV-1	1a	CTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAACATATGCAACAG
HCV-J	1b	-----A-----T-----G-----
HC-J6	2a	-----C-----GA-A-C-----G-----G-T-T-----
HC-J8	2b	-----A-C-T-TA-----C-----G-----GA-A-T-C-----
NE92	2d	-----C-----GA-A-----GA-A-----
NZL1	3a	-----C-----GA-CC-T-----GA-A-T-TC-----
HCV-TR	3b	-----C-T-----T-GA-CA-T-GG-----A-----
GB809	4e	-----A-C-T-TA-C-G-----GA-C-----C-----
CAM600	4e	-----A-----T-TA-C-G-----GA-C-T-----
GB724	4?	-----A-----A-C-G-G-----GA-T-----N-G-----
BE95	5a	-----C-A-C-T-GA-C-T-G-----G-A-----

Figure 4

	SEQ ID NO		379	428
HCV-1	1a	ACGTGGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTGGCGGCC		
HCVB1	1a	-----		
HCVHCT18	1a	-----T-----		
HCVHCT23	1a	-----		
HCVHCT27	1a	-----T-----		
HCVTH	1a	-----		
HCV-J	1b	-A-----T-----T-----		
HC-J6	2a	-----T-----C-TG-----A-----		
HC-J8	2b	-T-T-----C-TG-----T-----		
NE92	2d	-T-----C-TG-----		
HD10	3a	-----T-----T-----		
BR33	3a	-----T-----T-----		
BR36	3a	-----T-----T-----		
NZL15	3a	-----A-----C-----T-----		
HCV-TR	3b	-T-A-----T-----		
GB809_4	4a	-----A-----C-----G-----		
GB116	4c	-C-----T-----C-----A-----		
GB215	4c	-T-----T-----C-----A-----		
GB358	4c	-T-----T-----C-----A-----		
GB809_2	4e	-A-----A-----C-----T-A-----		
CAM600	4e	-A-----A-----C-----T-A-----		
CAMG22	4f	-A-----A-----C-----T-G-----		
CAMG27	4f	-----T-C-----C-----A-----		
GB549	4g	-----T-----A-----C-----G-----		
GB438	4h	-----G-----A-----C-----G-----		
CAR4/1205	4i	-C-----A-----C-----A-----		

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Figure 4 - Continued 1

CAR4/901	4?	181	G-----T-----A-----C-----A-----
BE95	5a	143	-----A-----T-----C-----A-----G-----
BE100	5a	195	-----A-----G-----C-----A-----G-----

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Figure 4 : Continued 3

CAR4/901	4?	CG-G--T-----TC-----A-----C--T--TA---C-G---G-
BE95	5a	CG-----G---TC--A-----T--C--A--C--T--GA---C--T--G-
BE100	5a	CG-----G---TC--A-----T--C--A--C--T--GA---T--G-

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Figure 4 : Continued 4

	479	ACGGCGTGAACATATGCACAGGGAACTTCTCGTTGCTCTTTCTCTATC	528
HCV-1	1a	-----	-----
HCV-EC1	1a	-----	-----
HCVHCT18	1a	-----	-----
HCVHCT23	1a	-----	-----
HCVHCT27	1a	-----	-----
HCVTH	1a	-----	-----
HCV-J	1b	-----	-----
		-----	-----
HC-J6	2a	-----	-----
HC-J8	2b	-----	-----
NE92	2d	-----	-----
		-----	-----
HD10	3a	-----	-----
BR33	3a	-----	-----
BR36	3a	-----	-----
NZL15	3a	-----	-----
HCV-TR	3b	-----	-----
		-----	-----
GB809_4	4a	-----	-----
GB116	4c	-----	-----
GB215	4c	-----	-----
GB358	4c	-----	-----
GB809_2	4e	-----	-----
CAM600	4e	-----	-----
		-----	-----
CAMG22	4f	-----	-----
CAMG27	4f	-----	-----
GB549	4g	-----	-----
GB438	4h	-----	-----

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Figure 4 - Continued 5

CAR4/1205	4i	---	GA-C-T-	---	T-	---
CAR4/901	4?	---	GA-T-	---	T-	---
BE95	5a	---	G-A-	---	TT-A-C	---
BE100	5a	---	G-	---	T-G	---

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Figure 4 - Continued 7

GB809_4	4a	529	578
Z4	4a	-----C-----A-T-T-G---C-C-----C-A-G-A-TG-G-	G-G--
Z1	4b		GTG--
GB116	4C	-C-CT-----A-T-T-G---C-----T--A-C-A--GT-A-	
GB215	4C	-A-CT-----A-T-T-G---C-----T--A-C--AT--	
GB358	4C	---CT-----A-T-T-G---C-----T--A-C--GT-A-	
Z6	4C		GTTA-
Z7	4C		GT-A-
DK13	4d		---A-
GB809_2	4e	---CT-----A-T-T-G---C-C---T---G---G-GTTA-	
CAM600	4e	---CT-----G-C---G-C---T---A-A---GTTA-	
G22	4f	---A-T-T-G---C---C---C---C---TGTG-	
G27	4f	---A-T-T-G---C---C---C---C---A-TGTG-	
GB549	4g	---A-A-T-T-G---C---C---C---C---GC-G-	
GB438	4h	---CT--TA-T-T-GC-C-A---C-A-G-T-TC-G-	
CAR4/1205	4i	-C-----T-AA-T-T-G-C---T---C-A--AT-	
CAR4/901	4?	-N-----A-T-T-G---C---C---C---C---TC-G-	
BE95	5a	---TA---T-T-T---G-TC---C---T-G-C-C-T-AGTT-C	
BE100	5a	---A---T-A-T---G---C-C---C---C---T-AGTT-C	
SA4	5a		GTT-C

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Figure 4 - Continued 8

		579	628
HCV-1	1a	AGTGCACAACCTCCACGGGGCTTTACCA	CGTCACCAATGATTGCCCTAACT
HCV-1	1a	-----T-----	-----T-----
HCVHCT18	1a	-----T-----	-----T-----
HCVHCT23	1a	-----T-----	-----T-----
HCVHCT27	1a	-----T-----	-----T-----
HCVTH	1a	-----T-----	-----T-----
HCV-J	1b	GTGT-C--A-A--T--G-C-C--T-C--	
HC-J6	2a	---AAG---AT---GTACCGGC---ATG---G---C-C---A-C---TG	
HC-J8	2b	---CA-G---ATT-GTTCTAGC---T---C---T---T-A---A	
S83	2c	G---CAAGG---A---GGC-ACTCC---ATGCCG---C---T-C---	
NE92	2d	G---CAAG---A---GCA-CTC---ATG---A---C---AG---A	
HD10	3a	GTG---G---A-GT-T-C-C-C-TGT-C-T---C-C---TT-C---TA	
BR33	3a	GTG---G---TA-GT-T-C-C-C-TGT-C-T---C-C---TT-C---TA	
BR36	3a	GTG---G---TA-GT-T-C-C-C-TGT-C-T---C-C---TT-C---TA	
NZL15	3a	GTG---G---TA-GT-T-C-C-C-GT-C-T---C-C---TT-C---TA	
HCV-TR	3b	GTACACG---A-GT-T-C-C-A-TGTGC-T---C-C---T---TG	

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Figure 4 - Continued 9

GB809_4	4a	CTAC-G-TG-TT--CA-C-T-A--	579	CTAC-G-TG-TT--CA-C-T-A--	528
Z4	4a	CTAC-G-TG-TT--CA-C-T-A--		CTAC-G-TG-TT--CA-C-T-A--	
Z1	4b	CTAC-G-TG-TT--CG-C-T-T--		CTAC-G-TG-TT--CG-C-T-T--	
GB116	4c	CTAT--G-T--CG-C-T-TA--		CTAT--G-T--CG-C-T-TA--	
GB215	4c	CTAT--TG-T--CG-C-T--		CTAT--TG-T--CG-C-T--	
GB358	4c	CTAT--TG-T--CG-C-T-A--		CTAT--TG-T--CG-C-T-A--	
Z6	4c	CTAT--TG-T--CG-C-T--		CTAT--TG-T--CG-C-T--	
Z7	4c	CTAT-A--TG-T--CG-C-T-A--		CTAT-A--TG-T--CG-C-T-A--	
DK13	4d	CTAT--AG-T--TG-C-T--		CTAT--AG-T--TG-C-T--	
GB809_2	4e	CTAT--TG-TT--CG--T-A--		CTAT--TG-TT--CG--T-A--	
CAM600	4e	CTAT--TG-TT--CA-T-A--		CTAT--TG-TT--CA-T-A--	
G22	4f	TTAT-A--A-T--CA-C-T-A--		TTAT-A--A-T--CA-C-T-A--	
G27	4f	TTAT-A--A-T--CA-C-T-A--		TTAT-A--A-T--CA-C-T-A--	
GB549	4g	CTAC-G-AT-T--CA-T--		CTAC-G-AT-T--CA-T--	
GB438	4h	CTAC-G-TG-AT--CA-C-T--		CTAC-G-TG-AT--CA-C-T--	
CAR4/1205	4i	CTAT--TG-TT--ACGG-TT-TA--		CTAT--TG-TT--ACGG-TT-TA--	
CAR4/901	4?	CTAC-G-TGT-T--CA-C--		CTAC-G-TGT-T--CA-C--	
BE95	5a	CTAC-A-TG-T-T--A--T-T-T--		CTAC-A-TG-T-T--A--T-T-T--	
BE100	5a	CTAC-A-TG-T-T--A-C-T-T--		CTAC-A-TG-T-T--A-C-T-T--	
SA4	5a	CTAC-A-G-T-T--G--T-T--		CTAC-A-G-T-T--G--T-T--	

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Figure 4 - Continued 10

HCV-1	1a	629	CGAGTATTGTGTACGAGGCGCGCATGCCATCTGCACTCCGGGGTGC	678
HVCEC1	1a		-----C-----T	
HCVHCT18	1a		-----A-----C-----T	
HCVHCT23	1a		-----A-----G-----T	
HCVHCT27	1a		-----A-----CA-----A-----T	
HCVTH	1a		-----T-----T-----G-----T	
HCV-J	1b		-A-----T-----A-G-CATG-----A-----C-C-----	
HC-J6	2a		AT-C---ACC-GGC-ACTCCAG-C---TG---C---GTC---C-----	
HC-J8	2b		AC-C---CACC-GGC---CTCA-T---C---AG-T---C---TCT---T---A---	
S83	2c		-T---C---T-GGC---CTT-AA-GA---AG-G---T---T---T---A---	
NE92	2d		GT-C---C---C-GGC---CTCAGG---TG-T-T---GTC---C-----T	
HD10	3a		GC-----T---C-AT---C-TT-T---T---A-C-C-C-T	
BR33	3a		GT-----T---C-AT---C-TT-T---T---G-G-C-C-C-T	
BR36	3a		GC-----C-AT---C-TT-T---T---A-C-C-C	
NZL15	3a		GC-----T---C-AT---T---T---A-C-C-C-T	
HCV-TR	3b		G-C-C-----C-AA---TG---T---TTA---C-A---	

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Figure 4 - Continued 11

GB809 4.	4a	-C--CG-A--C--T--AA-T-A-C-CCAT--AT--TTG-----	678
Z4	4a	-C---A-C-T-A--T-A-C-CA---A--TTG-----	
Z1	4b	-C-C-A-----A--AGC-CCA--A--TTG-A-----T	
GB116	4c	-C-A-----T-A-T-CCA---A--CTC-T-----	
GB215	4c	-C-A-----C-A-C-CCA---A--CT--A-----	
GB358	4c	-C-A-----A-C-AGC-CCA---A--CTC-A-----T	
Z6	4c	-C-A-----T---C-AAC-CCAG--T-A--CTC-A-----	
Z7	4c	-C-AA-----T---C-AAC-CCA---A--CTC-A-----	
DK13	4d	-C-A-C-T--AA-C-ATT-CCA---T-A--CTC-----A	
GB809 2	4e	-C-A-----A-C-A-A-CA---T-A--CTC-A-----	
CAN600	4e	-A-C-A-----A-C-AAA-CA---T-A--CTC-A-----	
G22	4f	-T-C-A-C-TT---A-T-C-CA---T--CT--A-A-----	
G27	4f	-T-C-A-C-TT---A-AGC-CA---T--TCT--A-A-----	
GB549	4g	-T-----T-A-T-A-C-CAT--A--TCTA-A-----T	
GB438	4h	-C-----T-A-C-A-C-CA---A--CTA-C-----T	
CAR4/1205	4i	-T-C-A-----T-A-C-AGA-CCA---T--CT-----T	
CAR4/901	4?	-C-C-A-----T-A-C-ATC-CCA---A--TTA-A-----	
BE95	5a	-TTCC-A-C-T-----A-ATA-CCTG---A--G-A-T-T-----	
BE100	5a	-TTCC-A-C-T-----A-AT--CTG---A--G-A-T-C-----	
SA4	5a	-TTCC-A-T-----T-ATA-CCTG--T--TG-A-T-T-----	

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Figure 4 - Continued 12

		679	728
HCV-1	1a	GTCCCTTGGTTCGTGAGGGCAAGCCTCGAGGTGTTGGGTGGCGATGAC	
HVCEC1	1a	-----AC-----T-----	
HCVHCT18	1a	-----AC-----T-----G-----	
HCVHCT23	1a	-----C-----AT-----T-----A-----G-----	
HCVHCT27	1a	-----C-----T-----AA-----C-----G-----AG-----	
HCVTH	1a	-----C-----T-----	
HCV-J	1b	-G-C-----C-G-A-T-TTT--CC-T-C-----A--C-C-----	
HC-J6	2a	-----G-----AGAA-T--G-TA-A--TC-----C--A-AC-G-CT-	
HC-J8	2b	-----A--T-AGAA--TAATGG-A--T-CAT-C--A-ACAAG-A--	
S83	2c	-----T-AG--ACC-C--T--TC-A--C--G-TG-	
NE92	2d	-----T-AGGAGA-----ATA-CC-C-----A-AC-G-TT-	
HD10	3a	--A-----T--AG-C-T-TA-A--TGC--C--ACCC-AG----	
BR33	3a	--A-----T-C-AG-C-----TA-G-T-CA-C--ACCC-AG-A--	
BR36	3a	A-A-----T-C-AG-C-----TA-A-C-C--C--ACCC-AG--	
NZL15	3a	--A-----T-C-AG-C-----TA-A-T-C--C--ACCC-AG----	
HCV-TR	3b	--G-C-----CACAAACC-----CAA-ATCA--C--ACAA-G-CT-	

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Figure 4 - Continued 13

GB809_4	4a	679	728
Z4	4a	--A-C-----GA-G-CC-G-----TG--TC-T-C-----AC-C--G-A--	
Z1	4b	--A-C-T-GATGACT-G--A-A--C-T-C-----AC-C-G--	
GB116	4c	--C-T-G-GAC-AG-TA-T-TC-C-C-----C-CT--	
GB215	4c	T-A-C-----GA-G-TT-G-TCAG-AC-C-C-----CC-T-	
GB358	4c	T-A-C-T-GA-G-TT-G-TCAG-AC-T-----CC-CT-	
Z6	4c	T-A-C-----GA-G-TT-G-TCAG-AC-C-C-----CC-C-	
Z7	4c	T-G-C-T-GA-G-TT-G-TCAG-AC-C-C-----CC-T-	
DK13	4d	--A-C-T-GA-G-----G--CAG-AC-C-C-----CC-T-	
BE809_2	4e	--T-----GA-G-A-G--AAG-T-CA-C-----T-TC-C-	
CAM600	4e	--A-C-T-GAGACC-G--CAG-C-----CC-C-	
G22	4f	--A-C-T-GA-GACT-G--CAG-C-----CC-C-	
G27	4f	--T-AA-AACT-G--CAG-TC-C-----A-CT--	
GB549	4g	--C-T-GA-AACT-G--CAG-AC-A-C-----A-A-CT--	
GB438	4h	--G-----GA-AACC-G-A--C-C-C-----TC-TT-A-	
CAR4/1205	4i	--G-C-T-AA-AACT-G-T-T-----C-T-C-A-TC-TT-A-	
CAR4/901	4?	A-A-C-T-GAGACC-G-TCAG-C-C-----TC-C-	
		A-A-C-----GA-GACC-G--TT--C-C-C-----AT-TC--	
BE95	5a	--G-----T-CATGACA--T-T-TGAGT--A-C-----CCAA--T--	
BE100	5a	--G-----T-CA-GA-A-AT-T-TGAGT--C-----CCAA--T--	
SA4	5a	--G-----T-CA-GC-A-AT-T-T-AGT-A-C-----CCAA--C--	

Figure 4 - Continued 14

[illegible]

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Figure 4 - Continued 15

GB809_4	4a	A-----TG--GTATCCATGG--CGCT--GCTCGA--TCCT-C--G-	778
Z4	4a	G-----A-----TGT-GCAC-CCCGGGCGCT--GCTTGA--TC-T-C-G-	
Z1	4b	---C-T-----G-GCCT--CC---CGCA--GTTAGA--TCCA-G--CA	
GB116	4c	T--C-C-----GG-GCCTT-C-TTGGTGCT--GCTAGAATCC--C--GA	
GB215	4c	T--C-C-----GG-GCCTT-CAT-GGTGCT--A-TTGAATCCT-C--GA	
GB358	4c	T--C-C-----GG-GCCTT-CAT-GGCGCT--GCTTGAATCC--C--GA	
Z6	4c	T--C-C-----GGTGTCTT--AT--GGTGCT--GCTTGAATCC--C--GA	
Z7	4c	T--C-C-----GG-GCCTT--AT--GGTGCA--GCTTGAATCCA-C--GA	
DK13	4d	---C-C-----TG-GCAAC--CTG--TGCT--GCTTGA--TCTT-GA---	
GB809_2	4e	T--C-A-----GT-GCCTT-C-T-GGTGCT--GCTCGA--CCT-G-G-	
CAM600	4e	T--C-A--A--GT-GCCAT-C-C-GGTGCT--GCTTGA--CCT-G-G-	
G22	4f	---C---C-----G-GCCAT-CCTTGGCGCT--ACTCGA--TCCA-G-G-	
G27	4f	---T---G-GCCAC-CATTGGCGCT--ACTTGA--TCCA-G----	
GB549	4g	A--C-T-----TG--CCCT--TTGGCGG--GCTCGAATCCA-G-G-	
GB438	4h	A--C-T-A--GT--CCCT-CCT-GGGGCT--ACTT--TCTG-A-G-	
CAR4/1205	4i	---C---C-----GG--CCAC--CCTACGTGCT--GCTTT--TCCT-A--GG	
CAR4/901	4?	A-----T-----TG-TCCCT-CCT-GGGGCT--GCTT--TC---A-G-	
BE95	5a	-----AC--T-AG--CC-AGCCT-GG-GCAGT-A--G-T-CT-----GA	
BE100	5a	---C---C-T-AG--CC-AGCTT-GG-GCAGT-A--G-T-CC-----GA	
SA4	5a	---C---T--T-AG--CC-A--CT-GG-GCGGT-A--G-T-CT-----GA	

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Figure 4 - Continued 16

		779	828
HCV-1	1a	GTCA	CATCGATCGCTTGTGGGAGCGCCACCCCTCTGTTCGGCCCTCTAC
HCV-1	1a	-----	-----C-----
HCVHCT18	1a	-----	-----C-----T
HCVHCT23	1a	-----	-----C-----
HCVHCT27	1a	-----	-----T-----T
HCVTH	1a	-----	-----C-----
HCV-J	1b	-C--G--T--T--C--T--GCG--TG--T--	-C--TA-G--
HC-J6	2a	CG-----T--CA--G--GAT--TC--	-G--C--C--T--T--
HC-J8	2b	CA--G--CA--A--C--AAT--GCA--T--GGC--C--	-T--G--T--
S83	2c	CA-----A--CA--C--GAT--TCT--T--GG--	-T--T--T--
NE92	2d	CG--T--T--ACCA--CA--T--CATC--T--GT--T--C--T--	-G--
HD10	3a	-G--TG--A--CA--T--G--G--CGCG--	-GA--G--C--T--T--
BR33	3a	---TG--G--C--T--A--A--CGCG--	-GA--G--C--T--G--T--
BR36	3a	---TG--G--C--AT--A--G--CGCG--	-GA--G--C--T--G--
NZL15	3a	---TG--G--C--AT--A--A--CGCG--	-GA--G--C--T--G--
HCV-TR	3b	CC--TG--G--A--G--A--CGCAGACAA--G--	-G--

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Figure 4 - Continued 17

GB809 4	4a	-G-TG-G-C-AA-G-A-TGCG-----G-G-----T-T-----T	828
Z4	4a	-A-TG-G-CT-AA-G-A-CGCG-----TT-G-----T-----T	
Z1	4b	-G-TG-A-C-A-G-G-TGCG-T-TA-G-----C-----T-----	
GB116	4c	---TG-G-----A-G-A-TGCT-T-TG-G-C-C-T-T-----	
GB215	4c	-A--G-G-CA-A-G-G-CGCT-T-TG-G-C-C-T-T-----T	
GB358	4c	---TG-G-----A-G-A-TGC-T-T-TGCG-C-C-T-T-----	
Z6	4c	-A-TG-G-C-A-G-G-CGC-T-TG-A-C-T-----	
Z7	4c	-A-TG-G-C-A-G-A-CGCT-T-AG-G-C-C-T-----	
DK13	4d	---G-G-----A-G-G-CG-----T-----C-C-----	
GB809 2	4e	-C-TG-G-C-A-G-A-TGCT-----G-G-C-C-----	
CAM600	4e	---TG-G-C-A-G-A-TGCT-----A-G-----C-----	
G22	4f	---G-G-T-A-G-G-C-CT-T-AT-G-C-A-A-----	
G27	4f	---G-G-T-A-G-A-C-CT-----AT-G-C-C-A-----	
GB549	4g	-G--G-G-CT-AA-G-G-TGC-----G-----C-----G-----	
GB438	4h	AG-TG-G-C-A-G-G-GCG-----T-A-C-T-----	
CAR4/1205	4i	CG--TG-G-C-AA-G-G-GC-----GGCA-C-C-TT-T-----	
CAR4/901	4?	-G-TG-G-T-A-G-G-TGCA-----T-C-T-----	
BE95	5a	-AGC-G-T-CTAC--A-CG-AG-G-TG-----C-C-GT-A-----	
BE100	5a	-AGC-G-T---TACT-G-G-AG-G-TG-----C-C-GT-A-----	
SA4	5a	-GGC-G-T-CTACT-A-CG-AG-G-TG-----C-C-C-A-----	

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Figure 4 - Continued 18

		829		878
HCV-1	1a	GTGGGGACCTATGCGGGTCTGTCTTCTTGTGCGCCAACTGTTACCTT		
HCVEC1	1a	-----G-----C-----T-----T-----		
HCVHCT18	1a	-----T-G-----T-----T-----		
HCVHCT23	1a	-----T-----CA-----T-----T-----		
HCVHCT27	1a	-----T-G-----T-----T-----T-----		
HCVTH	1a	-----G-----CA-----T-----T-----		
HCV-J	1b	-----T-C-----A-C-T-----C-TC-G-----		
HC-J6	2a	-----C-----TGGG-GA-G-----CA-C-----TTG-		
HC-J8	2b	-----A-TG-G-----G-C-GA-GA-C-ATCG-GGCT-----TGG-		
S83	2c	-----G-G-T-CG-GC-GA-G-G-C-CT-GG-CG-GT-G-		
NE92	2d	A-A-A-----G-T-CG-G-GA-GT-G-CTTCT-G-C-----T-A-		
HD10	3a	-----T-TA-G-T-----G-C-----C-C-G-A-----GCC-		
BR33	3a	-----T-TA-G-T-----G-C-----C-C-G-A-----GCC-		
BR36	3a	-----T-A-G-T-----G-----C-C-G-A-----GCC-		
NZL15	3a	-----T-TA-G-T-----G-----C-C-G-A-----GCC-		
HCV-TR	3b	-----C-----GCT-T-----G-----G-----G-A-----GC-		

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Figure 4 - Continued 19

GB809_4	4a	829	--T-A--C-T-AGG-CT-C-A-G-G-GA	878
Z4	4a		--T-----C-----AGG-C-C-GA-G-G-A--T-	
Z1	4b		A-T-A-T-G-T-AGG-C-C-A-G-G-GA	
GB116	4c		A-C-----G-----TGGC-A-T-G-T-T-GA--TT-T-	
GB215	4c		A-T-----T-G-T-TGGC-A-CT-G-T-T-GA--TT-T-	
GB358	4c		A-C-A-----G-----TGGC-A-T-G-T-T-GA--T-T-	
Z6	4c		--T-A-T-G-----TGG-CA-CT-G-T-T-GA--T-	
Z7	4c		A-T-----G-----TGGC-A-T-G-T-T-GA--TT-T-	
DK13	4d		A-C-A--G-G-T--GG--G-CT-G--T-----	
GB809_2	4e		--C-C--G-----TGGCT-A-CT-G-A--A--	
CAM600	4e		A-C-C--T-G-----TGGCT-A-CT-G-G--A--	
G22	4f		--T-----G-----GGCA-A-C-A-CG--GA--	
G27	4f		A-T-A-T-G-----AGGCA-A--A-G--GA--A-	
GB549	4g		A-C-A--T-----AGG-----C-G--G-GA--	
GB438	4h		A-C-A--AT-----AGG-----CT-G-CA-G-GA-G--GT-	
CAR4/1205	4i		A-T-A-T-G-----GG--G--T-G-CG--TA--	
CAR4/901	4?		--C-A-----C-T-AGG-----C-A-G-A-GA--	
BE95	5a		--A-A--GGG-T--G-AC-A-CT-G-A--A--A-	
BE100	5a		--T-A--GGG-T--G-AC-A-T-G-A--A--A-	
SA4	5a		--C-----GGG-----G-A-G-T-G-A--A--A-	

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Figure 4 - Continued 20

		879	928
HCV-1	1a	CTCTCCAGGCGCCACTGGACGACGCAAGGTGCAATTGCTCTATCTATC	
HVCEC1	1a	-----	
HCVHCT18	1a	-----	
HCVHCT23	1a	-----G-AC-----C-T-----	
HCVHCT27	1a	-----A-----A-----C-----C-----	
HCVTH	1a	-----	
HCV-J	1b	---A-TC-C-GT-TGA---GTA---A-----A-----	
HC-J6	2a	---G-ACA-A-----TTTGT-----AC-----C-----C-----	
HC-J8	2b	A-A-ACAA-----AACTTC-C-----AG-----C-T-C-----C-----	
S83	2c	G-G-ACAA-A---TAC-TTTGTTC-G-AA-----C-T-C-A-A-C-----	
NE92	2d	---G---CA-AT---TAA-TTTGTTC-G-AC-----C-T-C-A-A-C-----	
HD10	3a	-AGA-TC-T-----TCAA---GTC--GACC-T-T-C-----AC-G-G-C-----	
BR33	3a	-AGA--C-C-----TCAA---GTC--GACC-T-T-C-----GC-G-C-----	
BR36	3a	-AGA-TC-T-----TCAA---GTC--GACC-T-T-C-----GC-G-C-----	
NZLI5	3a	-AGA-TC-A-----TCAA---GTC--GACC-T-T-C-----GC-G-C-----	
HCV-TR	3b	-AGA-TC-C-----AC---CGT---GACG---C-----G-A-A-C-----	

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Figure 4 - Continued 21

GB809 4	4a	-CAG-GC-T-----C---G-A--T-----C-----A	879	928
Z4	4a	TCGG-GC-T-----C---G-AG-----T-C-----CA		
Z1	4b	-CGA-GC-C-G-----C-C-G-A-----C-----C		
GB116	4c	-CAG-GC-A-----C---G-AC-----T-C-----CG		
GB215	4c	-CGG-AC-A-----T---G-AC-----T-C-----CG		
GB358	4c	-CAG-GC-----T---G-AC-----T-C-----CG		
Z6	4c	-CAG-GC-A-----T---G-AC-----T-C-----CG		
Z7	4c	-CAG-GC-A-----T---G-AC-----T-C-----G		
DK13	4d	-CAA-TC-C-----C-C-AC-----T-C-----CA		
GB809 2	4e	-CAA-GC-A-----C-G-AC-T-----T-C-----CG		
CAM600	4e	-CAA-GC-A-T-----C-T-G-AC-----T-C-----CA		
G22	4f	-CGG-C-C-T-T-----C-C-G-AG-----T-C-C-----		
G27	4f	-AGG-C-C-TG-----C-C-G-AG-----T-C-----		
GB549	4g	-CGG-GC-C-----T---T-C-G-AC-----C-----G		
GB438	4h	-CAA-C-----T---T-C-G-A-----C-T-C-----G		
CAR4/1205	4i	-CGG-AC-CATT-TGAA-C-T-G-AC-----C-----CT		
CAR4/901	4?	-CAG-GC-C-----C-T-G-AC-----C-----C-T-CG		
BE95	5a	TAGG--TC-C-AG--GCT--GT--GAAC-----C-T-C-T-CA		
BE100	5a	TAGG--TC-C-AG-TGCT--GT--G-AC-----C-T-C-----CA		
SA4	5a	TAGG--TC-C-AG--ACT--GT--AC-----T-T-C-----		

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Figure 4 - Continued 22

HCV-1	1a	929	CCGGCCATATAACGGGTACCGCATGGCA	957
HCVHCT18	1a		-----C-----G-----	
HCVHCT23	1a		-----	
HCVHCT27	1a		-----A-----	
HCVTH	1a		-----	
HCV-J	1b		-----CG--T-A-----T	
HC-J6	2a		-T--TACC--C--T--A-----G	
HC-J8	2b		AA--T--C--C--C--C--T-----	
S83	2c		-G--GC--T--A-----T	
NE92	2d		-A-----C--C--T--A--T--G-----G	
HD10	3a		-A-----C--TT--A--A-----A-----T	
BR33	3a		-A-----C--TT--A--A--T--A-----T	
BR36	3a		-A-----C--TT--A--A--T--A-----T	
NZL15	3a		-A-----C--TT--A--A--T--A-----T	
HCV-TR	3b		-A-----G--TT--A--A--T--T-----G	

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Figure 4 - Continued 23

GB809 ₄	4a	929	-T-----C-C-C--A-G----	957	-G
Z4	4a		-T-----C-C-C--A-G----		-G
Z1	4b		-T-T-CG-CT--C-C-A-G----		-C
GB116	4c		-G-G-CG-T--C-C-A-G----		-
GB215	4c		-G-G-C-C-T-C-C-G-A----		-
GB358	4c		-G-G-CG-T--C-C-A-G----		-
Z6	4c		-A-G--C--C-C-A-G----		-
Z7	4c		-G-G-CG-T-A-C--A-A----		-
DK13	4d		-A-A--C-A-A--A-A----		-T
GB809 ₂	4e		-A-G--T--C-T-G----		-T
CAM600	4e		-G--C-T--T-G----		-
G22	4f		-G--C-C--TA-A----		-G
G27	4f		-A--C-C--A-A----		-G
GB549	4g		AT--C-C-C--TA-A----		-T
GB438	4h		TG--C-C-C--A-G----		-C
CAR4/1205	4i		-A-G-C-C----		-
CAR4/901	4?		T-----C-C-A-C--A-A----		-T
BE95	5a		GT-----G-T-C-C--G----		-G
BE100	5a		GT-----CG-C-C-C-T-AG----		-
SA4	5a		GT-----C-C-C--G----		-

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Figure 5

	SEQ ID	1
HCV1	1a	MSTNPKPQKKNKRNTRRRPQDVKFPGGGQIVGGVYLLPRRGRLGVRATR
HCVJ	1b	-----R-T-----
HCJ6	2a	-----R-T-----
HCJ8	2b	-----R-T-----
NE92	2d	-----R-T-----
	144	
EB1	3a	-----R-T-----I-----V-----C-----
NZL1	3a	-----L-----R-T-----I-----V-----
HCV-TR	3b	-----L-----RQT-----L-----N-----V-----V-----
BE98	3c	-----L-----R-T-----X-----V-----Q-----V-----
	148	
GB358	4c	-----R-T-----M-----
GB809	4e	-----L-R-T-----M-----
CAM600	4e	-----R-T-----M-----
GB724	4?	-----R-T-----M-----
EG-29	4?	R-----M-----
BE95	5a	-----R-T-----M-----
	152	

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Figure 5 - Continued 1

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				V-core	
HCV1	1a	KTSESRQPRRRQPIPKAR	RPEGRTHAQ	PGYPWPPLYGNEGCGWAGWLLSP	
HCVJ	1b	-----	-----	-----M-----	
HCJ6	2a	-----D-----	-ST-KS-GK	-----L-----	
HCJ8	2b	-----D-----	-ST-KS-GK	-----L-----	
NE92	2d	-----D-----	-T-KS-GK	-----L-----	
EB1	3a	-----	-S--S--	-----	
NZL1	3a	-----	-S--S--	-----	
HCV-TR	3b	-----KQ-HL-----	SR--S--	-----K--L-----	
BE98	3c	-----S-----R	-T--S--	-----	
GB358	4c	-----	-S--S--	-----	
GB809	4e	-----	-S--S--	-----	
CAM600	4e	-----	-T--S--	-----	
GB724	4?	-----	-S--S--	A-----	
EG-29	4?	-----	-S--S--	-----	
BE95	5a	-----	Q-T--S-G-	-----A--L-----	

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Figure 5 - Continued 2

		101	126
HCV1	1a	RGSRPSWGPTDPRRRSRNLGKVIDTL	
HCVJ	1b	-----	
HCJ6	2a	-----N-H-----V-----	
HCJ8	2b	-----T-----H-----R-----I-----	
NE92	2d	-----H-----	
NZL1	3a	-----N-----	
HCV-TR	3b	-----N-----F-----	
BE98	3c	-----N-----	
GB809	4e	-----N-----	
CAM600	4e	-X-X-N-X-	
GB724	4?	-----N-----	
BE95	5a	-----N-----K-----	

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Figure 5 - Continued 3

	127	176
	TCGFADLMGYTPLVGAPLGGAARALAHGVRVLEGDVNYATGNLPGCSFSI	
HCV-1	1a	
HCEC1	1a	
HCVHCT18	1a	
HCVHCT23	1a	
HCVHCT27	1a	
HCVTH	1a	
HCV-J	1b	
HC-J6	2a	
HC-J8	2b	
NE92	2d	
HD10	3a	
BR33	3a	
BR36	3a	
NZL1	3a	
HCV-TR	3b	

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Figure 5 - Continued 4

		127		176
GB809_4	4a	-----V-V-----	AV--I-----	-----
GB116_4c	4c	-----V-V-----	E--AV--I-----	-----
GB215_4c	4c	-----V-V-----	E--AV--I-----	-----
GB358_4c	4c	-----V-V-----	AV--I-----	-----
GB809_2	4e	-----V-V-----	AV--I-----	-----
CAM600_4e	4e	-----V-V-----	AV--I-----	-----
CAMG22_4f	4f	-----V-V-----	AV--I-----	-----
CAMG27_4f	4f	-----V-V-----	AV--I-----	-----
GB549_4g	4g	-----V-V-----	AV--I-----	-----
GB438_4h	4h	-----V-V-----	AV--I-----	-----
CAR4/1205_4i	4i	-----V-V-----	A--I-----	-----
CAR4/901_4?	4?	A-----V-V-----	AV--I-----	-----
BE95_5a	5a	-----G-V-V-----	-----P-----	-----
BE100_5a	5a	-----V-----G-V-V-----	-----	-----

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Figure 5 - Continued 5

	177	E1 ↓	V1		V2	226
HCV-1	1a	FLLALLSCLTPASA	YQVRNSTGLYHV	TNDPCNSSI	VYEAADAILHT	PGC
HCEC1	1a	-----	-----S-----	-----	-----	-----
HCVHCT18	1a	-----	H-----	-----	-----	-----
HCVHCT23	1a	-----	-----	-----	-----A-----	-----
HCVHCT27	1a	-----	-----S-I-----	-----	-----T-T--S-----	-----
HCVTH	1a	-----	-----	-----	-----A-----	-----
HCV-J	1b	-----I-----	-E--VS-I-----	-----S-----	-----M-M-----	-----
HC-J6	2a	-----I-T-V-----	AE-K-ISTG-M-----	-----T-D-----	TWQLQA-V-V-----	-----
HC-J8	2b	-----V--V-----	VE--I-SSS-YA-----	-----S-N-----	TWQLT--V--L-----	-----
S83	2c	-----	VE-KDTGDS-MP-----	-----S-----	-WLEG-V-----	-----
NE92	2d	-----I--V-G-----	L-K-TSSS-M-----	-----Q-----	-WQLR-V-V-----	-----
HD10	3a	-----F--IH--AS-----	LEW--TS--VL-----	-----S-----	-----D-V-----	-----
BR33	3a	-----F--IH--AG-----	LEW--TS--VL-----	-----S-----	-----D-V--A-----	-----
BR36	3a	-----F--IH--AS-----	LEW--TS--VL-----	-----S-----	-----D-V-----	-----
NZL1	3a	-----F--IH--AS-----	LEW--TS--VL-----	-----S-----	-----D-V-----	-----
HCV-TR	3b	-----F--C--G-----	LEYT-TS--VL-----	-----S-G-----	-----E-V--L-----	-----

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Figure 5 - Continued 8

	227	V3	V4	PUTATIVE	276
GB809_4	4a	--A-V---TPV	AVSND-LES	F---V-	-M-A-V-V-
Z4	4a	-MT-T---TPV	VAHPGA-LES	F---V-	-M-A-V-
Z1	4b	-TE-T---PL	APYPNA-LES	M---V-	-M-A-M--F-
GB116	4c	--V-Q---L	APVGA-LES	-S-V-	-M-A-V-
GB215	4c	-V-Q---L	APYGA-VES	F---V-	MM-A-V-
GB358	4c	-V-Q---L	APYGA-LES	-S-V-	-M-A-A-
Z6	4c	-V-Q---L	VSYGA-LDS	-S-V-	-M-A-V-
Z7	4c	---Q---L	APYGA-LES	I---V-	-M-A-V-
DK13	4d	---K-T---SL	AQHLNA-LES	---V-	-M-G-
GB809_2	4e	-KT-Q---L	SPVGA-LEP	---V-	-M-A-V-
CAM600	4e	-T-Q---L	SPVGA-LEP	---V-	-M-A-M-
CAMG22	4f	-T-Q---L	APYGA-LES	M---V-	-M-T-
CAMG27	4f	-T-Q---L	APYGA-LES	M---V-	-M-T-
GB549	4g	-T-T---PL	APVGA-LES	M---V-	-M-A-V-
GB438	4h	-T-V---IPL	VPLGA-L-S	V-Q-V-	-M-A-
CAR4/1205	4i	-KT-Q---L	APHLRA-LSS	-A-V-	-M-A-A--F-
CAR4/901	4?	-T-V---SL	APYGA-L-S	---V-	-M-A-
BE95	5a	-MT-V---QI	APSLGAVTAP	---AV-	Y-A-G-A-
BE100	5a	-KD-V---QI	APSFGAVTAP	---AV-	Y---G-A-
SA4	5a	--QD-V-K---QI	APNLGAVTAP	---AV-	Y-A-G-A-
HK2	6a	--VDDR-T---H-V	IPNAST---G	F---V-	--A-A-VV--S-

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Figure 5 - Continued 9

	277	TRANSMEMBRANE DOMAIN	V5	319
HCV-1	1a	VGDLGSLVFLVGQLFTF	SPRRHWTQG	CNCSIYPGHITGHRMA
HCV-1	1a	-----	-----	-----
HCV-18	1a	-----	-----	-----
HCV-23	1a	-----I-----	-----D-----	-----
HCV-27	1a	-----	-----D-----	-----
HCV-TH	1a	-----I-----	-----	-----
HCV-J	1b	-----S-----	-----YE-V-D-----	-----VS-----
HC-J6	2a	-----G-M-AA-M-IV-----	-----QH--FV-D-----	-----T-----
HC-J8	2b	---V--A-MILS-A-MV-----	---Q--NF-E-----	---Q-----
S83	2c	---V--ALM-AA-VVV-----	---QH-TFV-E-----	---R-----
NE92	2d	I-----A-M-AS-V-II-----	---QH-KFV-D-----	-----
HD10	3a	---M-A-----A-----	R---Q-V-T-----	---L---LS-----
BR33	3a	---M-A-----A-----	R---Q-V-T-----	---L---LS-----
BR36	3a	---M-A-----A-----	R---Q-V-T-----	---L---LS-----
NZL1	3a	---M-A-----A-----	R---Q-V-T-----	---L---LS-----
HCV-TR	3b	---AF-A-----A-----	R---T-V-T-----	---VS-----

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Figure 5 - Continued 10

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TRANSMEMBRANE
DOMAIN

V5

GB809_4	4a	----	GA	----	M	----	Q	----	D	----	T	----
Z4	4a	----	GA	----	M-MI	----	R	----	E	----	T	----
Z1	4b	----	G	----		D	R	----	D	----	VS	----
GB116	4c	I	G	----	M	S	Q	----	D	----	A-V	----
GB215	4c	I	G	----	M-S	S	R	----	D	----	A-V	----
GB358	4c	I	G	----	M-S	S	Q	----	D	----	A-V	----
Z6	4c	I	G	----	M-S	S	Q	----	D	----	A-V	----
Z7	4c	I	G	----	M-S	S	Q	----	D	----	A-V	----
DK13	4d	I	V	----	G		Q	----	D	----	T	----
GB809_2	4e	I	GL	----	N		Q	----	D	----	A	----
CAM600	4e	I	GL	----	M		Q	----	D	----	T	----
CAMG22	4f	----	GI	----	A-M		R	----	L	----	E	----
CAMG27	4f	I	GI	----	M	N	R	----	L	----	E	----
GB549	4g	I	G	----	M		R	----	D	----	D	----
GB438	4h	I	H	----	G-A-MV	S	Q	----	D	----	V	----
CAR4/1205	4i	I	G	----	A	I	R	----	I-E	----	S	----
CAR4/901	4?	----	G	----	M		Q	----	D	----	V	----
BE95	5a	----	A	----	AL	M	Y	----	Q-A-V-N	----	S-V	----
BE100	5a	----	A	----	AL	M	Y	----	Q-A-V-D	----	S-V	----
SA4	5a	----	A	----	A	M	Y	----	Q-T-V-D	----	S	----
HK2	6a	I	L	----	A		Q	----	V-D	----	T-V	----

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Figure 6

HCV-1	4648	4698
HCV-J	GTGTGCCAGGACCACTTTGAATTTTGGGAGGGCGTCTTTACAGGCCCTCACT	
HC-J6	--C-----C-A-G-C-----A-----C-----	
HC-J8	-----A-----G-----CA-T-C-C-----A	
HCC153	--A-T-A-----C-G-G-C-----A-CG-----T-----A	
EB1	-A-C-----A-----C-T-A-A-----	
EB2	↑	
EB6	4664	
EB7		
HCV-1	4699	4750
HCV-J	CATATAGATGCCCACTTCTATCCAGACAAGCAGAGTGGGGAGAACCTT	
HC-J6	--C-----CT-G-----C-A--GCA--A-C-----C	
HC-J8	--C-----C-T-----A-----ATCG-----A--TT-C	
HCC153	--C-T-C-----C-C-----G-----AG-A--A-A--T--	
EB1	--C-----G--A-----T-----CAG--ACTC--T-C	
EB2	-----CAG--ACTC--T-C	
EB6	A--CAG--ACTC--T-C	
EB7	A--CAG--ACTC--T-C	
	↑	4731

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Figure 6 - continued 1

	4751	4800
HCV-1	CCTTACCTGGTAGGTAACCAAGCCACGGTGTGCGTAGGGCTCAAGCCCC	
HCV-J	--C-----A-----A-----C-----G-T--	
HC-J6	G-A--T-AAC--C-----G-T-A-----CA-----	
HC-J8	G-G-T--AACG-C-----G--A-A-----C-----AA-G--	
HCC153	T-G-T---ACT-C-----T-----C-C-G-G-T---	
EB1	T-G-----AACT-C-----T-----CC-C-G-G-T-T	
EB2	T-G-----AACT-C-----T-----CC-C-G-G-T---	
EB6	T-G-----AACT-C-----T-----CC-C-G-G-T---	
EB7	T-G-----AACT-C-----T-----CC-C-G-G-T---	
	4801	4849
HCV-1	TCCCCCATCGTGGGACCACAGATGTGGAAGTGTGATTCGGCTCAAGCCCCA	
HCV-J	A--T-----A-----C-C-A-G-A-----	
HC-J6	C-----G-C-----GTC-----C-A-----	
HC-J8	--T-T-----GT-----C-A-C-A-G--A-T-	
HCC153	-----AGT-----G-----C-CG-A-G--T---A-	
EB1	-----AGT-----G-C-----A-C-CG-G-G-T---A-	
EB2	-----AGT-----G-C-----A-C-CG-G-A-----A-	
EB6	-----AGT-----G-----A-C-CG-G-G-----A-	
EB7	-----AGT-----G-----A-C-CG-G-G-----A-	

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Figure 6 - continued 2

	SEQ ID NO	4850	4900
HCV-1		CCCTCCATGGGCCAACACCCCTGCTATACAGACTGGCGCTGTTCAGAA	
HCV-J		-A-G-----G-----G-----G-A-A-C-----A--	
HC-J6		-A--GTG--C-C-----T-C-G--C-CT-----T-----ACC--C	
HC-J8		-A-GAC--T-C-C-----C-G--C-CT-----T-C-GACC--	
HCC153		-A-A-----A-T-G-T-T-----TC-GT-----GC-----C-A--	
HD10-1-25	29	↑	
HD10-1-3	31	4863	-C--A--
BR36-20-164	33		-C-A--
BR36-20-166	35		-C-A--
BR36-20-165	37		-C-A--
EB1	39		-C-A--
EB2		-A-A-C--A--T--G-----T-----TC	↑
EB6		-A-A-----A-T--G-----T-----TC	4892
EB7		-AT-A-----A-C-G-----T-----TC	
		↑	
		4878	

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Figure 6 - continued 3

	4901	4949
HCV-1	GAAATCACCCTGACGCCACCCAGTCACCAATACATCATGACATGTCATGTC	
HCV-J	--GG--T-C-A--CA-A--G--	
HC-J6	--GG--C--T-T-G-G--GCC-C--CA	
HC-J8	--GG--T--C-G-G--GCC-G--CA	
HCL153	--TG-T--A--CA-A--G--	
HD10-1-25	--TG-T--A--C--A--T-G--	
HD10-1-3	--TG-T--A--C--A--T-G--	
BR36-20-164	--TG-T--A--CA--A--G--	
BR36-20-166	--TG-T--A--CA--A--G--	
BR36-20-165	--TG-T--A--CA--A--G--	
	4950	4990
HCV-1	GGCCGACCTGGAGTCGTCACGAGCACCTGGGTGCTCGTTG	
HCV-J	--T--T--A--A--A--A--	
HC-J6	A--T--T--A-G-C--G--CT-A-C--	
HC-J8	A--T--C--A-A-G-A--T-A--C--G-CG-	
HCL153	A	
HD10-1-25	A--T--T--A-AAC--C--T-GC--	
HD10-1-3	A--T--T--A-AAC--C--T-GC--	
BR36-20-164	A--T--T--A-AAC--C--TT-GC--	
BR36-20-166	A--T--T--A-AAC--C--TT-GC--	
BR36-20-165	A--T--T--A-AAC--C--TT-GC--	

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Figure 6 - continued 4

		4991	5040
HCV-1		GGGGCTCCTGGCTGCTTTGGCCGGGTATGCTGTCAACAGGCTGCGTG	
HCV-J		----A---T-G-C---C-----C-----A-G-----A-----	
HC-J6		-G-G---T---G-CG-C---C-----G-G-C-G-T-T	
HC-J8		-G-G-G-A-C-CG---A-T-C-----G-G-T-----A-T	
HD10-1-25		-A-G-----C-G-CC-A-G-C-C---T-----GTC-----T	
HD10-1-3		-A-G-----C-G-CC-A-G-C-C---T-----GTC-----T	
BR36-20-164		-A-G-----C-G-CC-A-G-C-C---T-----GTC-T-T-T	
BR36-20-166		-A-G-----C-G-CC-A-G-C-C---T-----GTC-T-T-T	
BR36-20-165		-A-G-----C-G-CC-A-G-C-C---T-----GTC-T-T-T	
		5041	5090
HCV-1		GTCAATAGTGGCAGGTCGTCTTGTCCGGGAAGCCGGCAATCATACCTGA	
HCV-J		-----T-----A-A-----G---A---TG-T-T-T-C--	
HC-J6		TG--CA-C---C-CT-GCA-G-TAA-CA-CGAG-C-TCG-TGC---G--	
HC-J8		TC---CA-T---C-CC-ACA-C-AAT-ATCG-GT--TTG-GGCC--C--	
HD10-1-25		--A-C---TCATA--AGC--GGG-C-----C-G-T-A--	
HD10-1-3		--A-C---TCATA--AGC--GGG-C-----C-G-T-A--	
BR36-20-164		--G-T---TCATA--AGC--GGG-C-----G-T-A--	
BR36-20-166		--G-T---TCATA--AGC--GGG-C-----G-T-A--	
BR36-20-165		--G-T---TCATA--AGC--GGG-C-----G-T-A--	

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Figure 6 - continued 5

	5091	5140
HCV-1	CAGGGAAGTCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGC	
HCV-J	-----AG-----TG--TCA-	
HC-J6	-A--G-----TGAG-CT--T-----G--A--TG-CTCTA	
HC-J8	-A--A--T-A--TGAG-CC--T-----A--G-CTCCA	
HD10-1-25	-A--G--GT-G--T-A-C--A-----G-----G--AG	
HD10-1-3	-A--G--GT-G--T-A-C--A-----G-----G--AG	
BR36-20-164	-AA--G--GT-G--T-A-C-A-A-----A--AG	
BR36-20-166	-AA--G--GT-G--T-A-C-A-A-----A--AG	
BR36-20-165	-AA--G--GT-G--T-A-C-A-A-----A--AG	
	5141	5190
HCV-1	ACTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAGCAG	
HCV-J	--C-C-T-----A--CA-----A-----A--	
HC-J6	GAGCGG-TCT--T--AG-G--CA-CG-A-A-----AT-C-G--TCC	
HC-J8	-AGCCG-CCT--T--G-----CA-CG-A-G--G--AT-C--ATCT	
HD10-1-25	C-GCC--A-----A-----CTCA-G-AA-A--C-C-----G--	
HD10-1-3	C-GCC--A-----A-----CTCA-G-AA-A--C-C-----G--	
BR36-20-164	CTGCC--A--T-----A-----CTCA-G-AA-A--TC-C-----GGA	
BR36-20-166	CTGCC--A--T-----A-----CTCA-G-AA-A--TC-C-----G-A	
BR36-20-165	CTGCC--A--T-----A-----CTCA-G-AA-A--TC-C-----G-A	

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Figure 6 - Continued 6

	5191	5240
HCV-1	AAGGCCCTCGGCCTCCTGCAGACCGCTCCGTCAGGCAGAGGTTATCGC	
HCV-J	-----AT-G-----A-A--CA--AAG--A--G-----C-GCT--	
HC-J6	--AT-AA--T-AT-----CAA--T--AAA--A--TC-A-AC-ACA	
HC-J8	--ATA-AA-----A--ACAG--CA-AA-G--A--TC-A-AC-ACA	
HD10-1-25	--AAT--T-A-G-----CGA--CA--AA--ACA--CT--C--T-A	
HD10-1-3	--AAT--T-A-G-----CGA--CA--AA--ACA--CT--C--T-A	
BR36-20-164	--A-T--T-AT-G-----CGA--CA--AA--ACA--CT--C--T-A	
BR36-20-166	--A-T--T-AT-G-----CGA--CA--AA--ACA--CT--C--T-A	
BR36-20-165	--A-T--T-AT-G-----CGA--CA--AA--ACA--CT--C--T-A	
	5241	5290
HCV-1	CCCTGCTGTCCAGACCACACTGGCAAAACTCGAGACCTTCTGGGGAAGC	
HCV-J	T--C-TG--GG--T--G--G-GCC--T--GT-----A-	
HC-J6	A--C-----G--G-TTCT-----CC--GG-A--CAA-----C--A-	
HC-J8	G--A--A--A--T-ATCA--CC--G--T--ACAA--T-----C--A-	
HD10-1-25	G--C-TAA-AGCTT-----G--T--A-----CAC----	
HD10-1-3	G--C-TAA-AGCTT-----G--T--A-----CAC----	
BR36-20-164	G--CATA-AACT-----G--T--G--T--G--T--CAC----	
BR36-20-166	G--CATA-AACT-----G--T--G--T--G--T--CAC----	
BR36-20-165	G--CATA-AACT-----G--T--G--T--G--T--CAC----	

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Figure 6 - continued 7

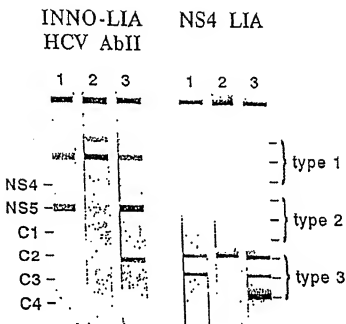
HCV-1	5292
HCV-J	AT
HC-J6	-C
HC-J8	-C
HD10-1-25	-C
HD10-1-3	--
BR36-20-164	--
BR36-20-166	--
BR36-20-165	--

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Figure 7

	SEQ ID NO	1290	1300	1310	1320	1330
HCV-1	1a	ITTGSPITYTYGKFLADGGCGGAYDIIICDECHSDATSI				LGIG
HC-V-J	1b	-----G-----C-----				S-T-----
HC-J6	2a	V--A-----A-----				AV-S-T-----
HC-J8	2b	V--DS-----I-----AA-----				V--T-----
BE95	5a	---AS-----T-----				q--T-----
	270					
		1340	1350	1360	1370	1380
HCV-1	1a	TVLDQAEATAGARLVLATATPPGSGVTVPHPNIEEVALSTTG				EIFPYGKAI
HC-V-J	1b	-----I-----				N-----
HC-J6	2a	---V--T-----T-----				GQE-----R-----
HC-J8	2b	---V-----T--T--S-----				GHE-----
BE95	5a	-----T-----				pQE--V--R-----

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Figure 9

	SEQ ID NO	
PC-3-4	49	1
PC-3-8	51	50
PC-2-1	41	
PC-2-6	43	
PC C/E1	53	
PC-3-4		51
PC-3-8		100
PC-2-1		
PC-2-6		
PC C/E1		

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Figure 9 - Continued 1

	101	150
PC-3-4	TTTACTTGTGGCGCGAGGGCCCTAGGATGGGTGTGGCGGGACTCGG	
PC-3-8	-----	
PC-2-1	-----	
PC-2-6	-----	
PC C/E1	-----	
	151	200
PC-3-4	AAGACTTCGGAACGGTCGCAACCCCGTGGACGGCGTCAGCCTATTCCTAA	
PC-3-8	-----	
PC-2-1	-----	
PC-2-6	-----	
PC C/E1	-----	

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Figure 9 - Continued 2

	201	250
PC-3-4	GGCGGCCAGCCACGGCCGGTCCTGGGGTCAACCCGGGTACCCTTGGC	
PC-3-8	-----	
PC-2-1	-----	
PC-2-6	-----	
PC C/E1	-----	
	251	300
PC-3-4	CCCTTTACGCCAATGAGGGCCTCGGGTGGGCGAGGGTGGCTGCTCTCCCCT	
PC-3-8	-----	
PC-2-1	-----	
PC-2-6	-----	
PC C/E1	-----	

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Figure 9 - Continued 3

	301	350
PC-3-4	CGAGGCTCTGGCCTAATTGGGGCCCAATGACCCCGGCGAAATCGCG	
PC-3-8	-----	
PC-2-1	-----	
PC-2-6	-----	
PC C/E1	-----	
	351	400
PC-3-4	TAATTGGGTAAGGTCAATCGATACCCCTAACGTGCGGATTCGCCGATCTCA	
PC-3-8	-----	
PC-2-1	-----	
PC-2-6	-----	
PC C/E1	-----	

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Figure 9 - Continued 4

	401	450
PC-3-4	TGGGTATATCCCGCTCGTAGCGGGCCCCATTGGGGGCCGTCGCAAGGGCT	
PC-3-8	-----C-----G-----	
PC-2-1	-----	
PC-2-6	-----	
PC-4-1	-----	
PC-4-6	-----	
PC C/E1	-----Y-----R-----	
	SEQ ID NO	451
PC-3-4	CTCGCACACGGTGTGAGGTCCTTGAGGACGGGGTAAACTATGCAACAGG	500
PC-3-8	-----C-----	
PC-2-1	-----	
PC-2-6	-----	
PC-4-1	-----	
PC-4-6	-----	
PC C/E1	-----S-----	

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Figure 9 - Continued 5

PC-3-4	501	550
PC-3-8	GAATTACCGGTGCTCTTTCCTATCTTTATCTTGCTCTCTCTCGT	
PC-2-1	-----	-----
PC-2-6	-----	-----
PC-4-1	-----	-----
PC-4-6	-----	-----
PC C/E1	-----	-----
PC-3-4	551	600
PC-3-8	GTCTGACCGTTCGGCCTCTGCAGTCCCTACCGAAATGCCTCTGGGATT	
PC-4-1	-----	-----
PC-4-6	-----	-----
PC C/E1	-----	-----

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Figure 9 - Continued 6

	601	650
PC-3-4	TATCATGTTACCAATGATTGCCCAAACCTCTCCATAGTCTATGAGGCAGA	
PC-3-8	-----	
PC-4-1	-----	
PC-4-6	-----	
PC C/E1	-----	
	651	700
PC-3-4	TAACTGATCCTACACGCACCTGGTTGCGTGCCTTGTGTGTCATGACAGGTA	
PC-3-8	-----	
PC-4-1	-----	
PC-4-6	-----	
PC C/E1	-----	

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Figure 9 - Continued 7

	701	750
PC-3-4	ATGTGAGTAGATGCTGGGTCCAAATTACCCCTACACTGTCAGCCCCGAGC	
PC-3-8	-----	
PC-4-1	-----	
PC-4-6	-----	
PC C/E1	-----	
	751	800
PC-3-4	CTCGGAGCAGTCACGGCTCCTCTTCGGAGAGCCGTTGACTACCTAGCGGG	
PC-3-8	-----	
PC-4-1	-----	
PC-4-6	-----	
PC C/E1	-----	

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Figure 9 - Continued 8

	801	850
PC-3-4	AGGGGCTGCCCTCTGCTCCGCTTATACGTAGGAGACCGTGTGGGCA	
PC-3-8	-----	
PC-4-1	-----	
PC-4-6	-----	
PC C/E1	-----	
	851	900
PC-3-4	CTATTCTTGGTAGGCCAAATGTTACCTATAGGCCTCGCCAGCACGCTACG	
PC-3-8	-----	
PC-4-1	-----	
PC-4-6	-----	
PC C/E1	-----	

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Figure 9 - Continued 9

	901	950
PC-3-4	GTGGAAGCTGCAACTGTTCCATTTACAGTGGCCATGTTACCGGCCACCG	
PC-3-8	-----	
PC-4-1	-----	
PC-4-6	-----	
PC C/E1	-----	
	951	
	GATGGCA	
PC-3-4	-----	
PC-3-8	-----	
PC-4-1	-----	
PC-4-6	-----	
PC C/E1	-----	

Figure 10

	SEQ ID NO	
HCV-1	1a	3856
HCV-J	1b	3890
HC-J6	2a	ACCACTGGCAGCCCCATCACGTACTCCACCTACGG
HC-J8	2b	-----G-G-----TT-
PC1_37	5a	-----G-C-GGCG-----A-T-
PC1_48	5a	-----C-GGA-T-T-----T-T-
BR36	3a	-----C-AGCTT-T-----T-
		-----C-AGCTT-T-----T-----
HCV-1	1a	3891
HCV-J	1b	3940
HC-J6	2a	CAAGTTCCCTTGCCGACGGCGGGTGCTCGGGGGGCGCTTATGACATAATAA
HC-J8	2b	-----T-A-----C-----C-----C-----C-----C-----C-----
PC1_37	5a	-----A-----C-----T-G-C-----G-A-C-----C-----C-----C-----C-----
PC1_48	5a	-----TA-C-A-T-A-C-----TG-A-C-----T-C-----C-----C-----C-----
BR36	3a	-----T-T-A-----T-A-C-----GC-----G-G-C-----G-G-C-----
		-----T-T-A-----T-A-C-----G-----G-----G-----G-----C-----C-----
HCV-1	1a	3941
HCV-J	1b	3990
HC-J6	2a	TTTGTGACGAGTGCCTCCACGGATGCCACATCCATCTTGGGCATCGGC
HC-J8	2b	-----T-A-----A-T-CT-G-TA-----
PC1_37	5a	-----A-C-T-A-----TG-GT-----CT-T-CA-----TC-C-----A-----
PC1_48	5a	-----A-C-----T-AGT-----C-T-TA-----C-T-----T-A-----
BR36	3a	-----A-C-----T-CA-----C-CA-----TC-T-G-A-----
		-----A-C-----T-CA-----C-CA-----TC-T-G-A-----

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Figure 10 - Continued 1

		3991		4040
HCV-1	1a	ACTGTCCTTGACCAAGCAGAGACTCGGGGGCGGAGACTGGTTGTGCTCGC		
HCV-J	1b	--A--G-T-G--G-T-A--C-G-C-C--		
HC-J6	2a	--A--C-T--A-C--TC-G-AAC--A-G--		
HC-J8	2b	--A--T--C-A-C-TC-G-A-G-TT-G--		
PC1 37	5a	-----G-----G-T-A-T-G-C-C-CT-G--		
PC1_48	5a	-----G-----G-T-A-T-G-C-C-CT-G--		
BR36	3a			
		4041		4090
HCV-1	1a	CACCGCCACCCTCCGGGCTCCGTCACTGTGCCCCATCCCAACATCGAGG		
HCV-J	1b	-----G-----A-GA--C-----A-C--		
HC-J6	2a	T-G-T-G-C-C-G-A-G-AACC--C-----A--		
HC-J8	2b	--A--G--C-TA-G-G-AACT--CAGT--A--		
PC1 37	5a	--G-----C--AGT--G-AAC--C-----		
PC1_48	5a	--G-----C--AGT--G-AAC--C-----		
BR36	3a			
		4091		4140
HCV-1	1a	AGGTGCTCTGTCCACCACCGGAGAGATCCCTTTTACGGCAAGGCTATC		
HCV-J	1b	-A-G-C-----A-T-----T-C-C-T--A-C--		
HC-J6	2a	-----C-CGGCAGGAG-T-----C-C-T-G-G--G-T		
HC-J8	2b	-----G-C-TGGTCA-GAG-C-----T--A--T		
PC1 37	5a	-A-G-C--C-TCAGGAG--G--G-T-C-C--GA-C-T		
PC1_48	5a	-A-G-C--C-TCAGGAG--G--G-T-C-C--GA-C-T		
BR36	3a			

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Figure 10 - Continued 2

		4141			4190
HCV-1	1a	CCCCTCGAAGTAATCAAGGGGGGAGACATCTCATCTTCTGTCATTCAAA			
HCV-J	1b	---A-T-G-CC-----A-G-----C-----C-			
HC-J6	2a	---GTC-TAC-----A-A-----CT-G-----C-C-			
HC-J8	2b	---A-CTT-C-----C-----CT-G-----T-C-			
PC1_37	5a	---T-CTT-T-A-----T-T-G-----C-----C-			
PC1_48	5a	---T-CTT-T-A-----T-T-G-----C-----C-			
BR36	3a				
		4191			4240
HCV-1	1a	GAAGAAGTGCACGAACCTGCCGCAAGCTGTCGCATTGGGCATCAATG			
HCV-J	1b	-----T-----G-----ACA-GCC-C-AC-----			
HC-J6	2a	---A-----T-----G-----TGGG-GTA-----T-G-C-			
HC-J8	2b	-----G-----G-----A-GGCC-CCGG-GCA-----TG-			
PC1_37	5a	---A-A-T-T-----AAGC-A-----AC-AGCC-----G-G-C-			
PC1_48	5a	---A-A-T-T-----AAGC-A-----AC-AGCC-----G-G-C-			
BR36	3a				
		4241			4290
HCV-1	1a	CCGTGGCCTACTACCGGGTCTTTGACGTCTCCGTCTATCCCGACCAAGCGGC			
HCV-J	1b	-T-A-G-T-----G-----C-T-----A-----T-----A			
HC-J6	2a	-A-----A-----A-A-G-G-----C-----A-A-A-TCAG-A			
HC-J8	2b	---T-A-----TA-G-----C-----C-----T-A-A-TCAA-A			
PC1_37	5a	---A-T-TA-A-----A-----CG-----A-C-A-CA-A			
PC1_48	5a	---A-T-TA-A-----A-----CG-----A-C-A-CA-A			
BR36	3a				

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Figure 10 - Continued 3

4291
 HCV-1 1a GATTTGTGTCGTGGCAACCGATGCCCTCATGACCGGCTATACCGGCGA 4340
 HCV-J 1b --C-C-T--T--A-C-T-A--G-T-T--
 HC-J6 2a --C-A-G--C-C-C--G-G-T--T--A--
 HC-J8 2b --C-G-G--T-C-C-T--A--T-G-C--
 PC1_37 5a --C-G--GTGCAGC--C-G--G-A-TC--
 PC1_48 5a --C-G--GTGCAGC--C-G--G-A-TC--
 BR36 3a

4341
 HCV-1 1a CTTGCACTCGGTGATAGACTGCATACGTGTGTCAACCCAGACAGTCGATT 4390
 HCV-J 1b --T--A--C--C--A--
 HC-J6 2a --T--C--C--CGTAGCG--T-AGTT--A-C-
 HC-J8 2b --T--C--C--T--GTTGCA--T-T--TT--T-C-
 PC1_37 5a --T-T-T-C--CT-CGCC--T--G-G-C-
 PC1_48 5a --T-T-T-C--CT-CGCC--T--G-G-C-
 BR36 3a

4391
 HCV-1 1a TCAGCCTTGACCCCTACCTTCACCATTGAGACAATCACGCTCCCCCAGGAT 4440
 HCV-J 1b --T-G-T-C--G-CA--G--A-C-
 HC-J6 2a --T-G--C-A--AACC--CAG-TG--T-A-C-
 HC-J8 2b --A--A--CACC--TCAA--CG--T--C-
 PC1_37 5a --T-G-T-C-T-T--T-C--AG-G--C-
 PC1_48 5a --T-G-T-C-T-T--T-C--AG-G--C-
 BR36 3a

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Figure 10 - Continued 4

		4441			4490
HCV-1	1a	GCTGTCCTCCGCACTCAAGTCGGGAGGAGCTGGCAGGGGGAAGCCAGG			
HCV-J	1b	--G-G-G-TG-G-G-G-A-T-----C-G-AGT--			
HC-J6	2a	-----A-T-GC-G-C-----C-C-G-----A-GA-TG--			
HC-J8	2b	-----T-G-----A-A-G-A-----G-----CGATTG--			
PC1_37	5a	--A-G--A-A-GC-G-T-----C-C-G-G-A-T-G--AC--			
PC1_48	5a	--A-G--A-A-GC-G-A-----C-C-G-G-A-T-G--AC--			
BR36	3a				
		4491			4550
HCV-1	1a	CATCTACAGATTGTGGCACCAGGGGAGCGCCCTCCGGCATGTTCCGACT			
HCV-J	1b	-----G-----A-T-A-A-A-G-----A-----			
HC-J6	2a	T-T-T-G-A--TT-CA-T-T--AG--A-A--T--A			
HC-J8	2b	-G-T--G-A--TT-GT-A-C--A-G-G-T-G--A			
PC1_37	5a	---A--C-G-A--CT-GG-T-A--A-A-G-T-----			
PC1_48	5a	---A--C-G-A--CT-GG-T-A--A-A-N-T-A-----			
BR36	3a				
		4551			4590
HCV-1	1a	CGTCGCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGATGAGCTC			
HCV-J	1b	-C-G-----G-----C-----C-----			
HC-J6	2a	GTGTA-G-----C-----C-T-----GGCC-A-----			
HC-J8	2b	GGTA-G-----C-----T-C-GGCA-C-----C-----T			
PC1_37	5a	-CGTG-G-----C-----C-T-C-A-----C-T-G			
PC1_48	5a	-CGTG-G-----C-----C-T-C-A-----G-----T-G			
BR36	3a				

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Figure 10 - Continued 5

		4591		4640
HCV-1	1a	ACGCCCGCGGAGACTACAGT	AGGCTACGAGCGTACATGAACACCCCGGG	
HCV-J	1b	-----T-----CT-G-----T-G-G-T-----C-A-T-A-A-	-----T-----CT-G-----T-G-G-T-----C-A-T-A-A-	
HC-J6	2a	-----A-A-G-----C-C-C-----CA-A-TT-C-----A-T-	-----A-A-G-----C-C-C-----CA-A-TT-C-----A-T-	
HC-J8	2b	-----A-T-T-----G-G-A-C-G-T-TT-C-----G-C-	-----A-T-T-----G-G-A-C-G-T-TT-C-----G-C-	
PC1 37	5a	-----T-T-----C-G-T-G-C-T-N-A-----C-	-----T-T-----C-G-T-G-C-T-N-A-----C-	
PC1 48	5a	-----T-T-----C-G-T-G-C-T-----A-----C-	-----T-T-----C-G-T-G-C-T-----A-----C-	
BR36	3a			
		4641		4690
HCV-1	1a	GCTTCCCGTGTGCCAGGACCATCTTGAATTTTGGAGGCGTCTTTACAG	GCTTCCCGTGTGCCAGGACCATCTTGAATTTTGGAGGCGTCTTTACAG	
HCV-J	1b	-----T-G-----C-----C-A-G-C-----A-----C-	-----T-G-----C-----C-A-G-C-----A-----C-	
HC-J6	2a	TTT-G-----A-----A-----G-----CA-T-C-C-	TTT-G-----A-----A-----G-----CA-T-C-C-	
HC-J8	2b	-----TT-G-----A-T-A-----C-G-G-C-----A-CG-----	-----TT-G-----A-T-A-----C-G-G-C-----A-CG-----	
PC1 37	5a	-----C-T-C-T-----T-G-----C-----G-G-C-G-	-----C-T-C-T-----T-G-----C-----G-G-C-G-	
PC1 48	5a	-----C-T-C-T-----T-G-----C-----G-G-C-G-	-----C-T-C-T-----T-G-----C-----G-G-C-G-	
BR36	3a			
		4691		4740
HCV-1	1a	GCCTCACTCATATAGATGCCCACTTTCTATCCAGACAAAGCAGAGTGGG	GCCTCACTCATATAGATGCCCACTTTCTATCCAGACAAAGCAGAGTGGG	
HCV-J	1b	-----C-C-----C-----CT-G-----C-A-----GCA--A	-----C-C-----C-----CT-G-----C-A-----GCA--A	
HC-J6	2a	-----A-C-----C-----C-T-----A-----ATCG-----	-----A-C-----C-----C-T-----A-----ATCG-----	
HC-J8	2b	-----T-----A-C-T-C-----C-C-----G-----AG-A--A	-----T-----A-C-T-C-----C-C-----G-----AG-A--A	
PC1 37	5a	-----G-----A-C-C-C-T-----A-G-G-A-----C-A--G-----	-----G-----A-C-C-C-T-----A-G-G-A-----C-A--G-----	
PC1 48	5a	-----G-----A-C-C-C-T-----A-G-G-A-----C-A--G-----	-----G-----A-C-C-C-T-----A-G-G-A-----C-A--G-----	
BR36	3a	-----A-A-----C-----C-----G-A-----T-----CAG--A	-----A-A-----C-----C-----G-A-----T-----CAG--A	

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Figure 10 - Continued 6

		4741	4790
HCV-1	1a	GAGAACCTTCCTTACCTGCTAGCGTACCAAGCCACCGTGTGCGTAGGGC	
HCV-J	1b	-C-----C-C-----A-----A-----C-----	
HC-J6	2a	-A--TT-CG-A--T-AAC--C-----G-T-A-----	
HC-J8	2b	-A--T--G-G-T--AACG-C-----G-----A-A-----C-----	
PC1_37	5a	-----TT-C-A-----T-----A-A-C-T-T-C-C-----	
PC1_48	5a	-----TT-N-A-----T-----A-A-C-T-T-C-C-----	
BR36	3a	CTC---T-CT-G-T---ACT--C-----T-----C-C-----	
		4791	4840
HCV-1	1a	TCAAGCCCTCCCTCCATCGTGGACGAGATGTGGAAGTGTGATTGCGC	
HCV-J	1b	--G-T-A-T-----A-----C-C-A--G--	
HC-J6	2a	CA-----C-----G-C-----GTC-----C-A--A--G--	
HC-J8	2b	AA-G-----T-T-----GT-----C-A-C-A-G--	
PC1_37	5a	GA--G-C--C--CAGC--ACA-----A-CA-C-C-T--	
PC1_48	5a	GA--G-C--C--CAGC--ACA-----A-CA-C-C-T--	
BR36	3a	G-G-T-----AGT-----G-----C-CG-A--G--	
		4841	4890
HCV-1	1a	TCAAGCCACCTCCATGGGCCAACACCCCTGCTATACAGACTGGCGCT	
HCV-J	1b	-A-----A-G-----G-----G-----G-A--A--C--	
HC-J6	2a	-----A--GTG-C-C-----T-C-G--C-CT-----T--	
HC-J8	2b	-----A-T-A-GAC--T-C-C-----C-G--C-CT-----T-C--	
PC1_37	5a	-----A-G-NT-AAC--C-T-T-----CT-G-----G--GC-C--	
PC1_48	5a	-----A-G-TT-AAC--C-T-T-----CT-G-----G--GC-C--	
BR36	3a	-T-----A-A-A-----A-T-G-T-T-----TC-GT-----GC--	

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Figure 10 - Continued 7

		4891	4940
HCV-1	1a	GTTCAGAAATCAATCACCCTGACGCACCCAGTCACCAATACATCATGAC	
HCV-J	1b	---A---GG---T-C-A---CA-A---G-	
HC-J6	2a	---ACC-C-GG---C---T-T-G-G---GCC-	
HC-J8	2b	---GACC---GG---T---C-G-G---GCC-	
PC1_37	5a	---C---G---A---CA---G---T---G-	
PC1_48	5a	---C---N---G---A---CA---G---T---G-	
BR36	3a	---C-A---TG-T---A---CA---A---G-	
		4941	4990
HCV-1	1a	ATGCATGTCGGCCGACCTGGAGTCGTACGAGCACCTGGGTGCTCGTTG	
HCV-J	1b	---A---T---T---T---A---A-	
HC-J6	2a	C---CAA---T---A-G-C---G---CT-A-C-	
HC-J8	2b	G---CAA---T---C-A-A-G-A---T-A---C-G-CG-	
PC1_37	5a	T---T-G-T---A-T-C---T---T-G-G-	
PC1_48	5a	T---T-G-T---A-T-C-N---T---T-G-G-	
BR36	3a	---A-T-T---A-AAC---C---TT-GC-	
		5040	
HCV-1	1a	GCGGCTCCTGGCTGCTTTGGCCGGTATTGCCTGTCACAGGCTGCGTG	
HCV-J	1b	---A---T-G-C---C---A-G---A-	
HC-J6	2a	-G-G-T---G-CG-C---C---G-G-C-G-T-T-	
HC-J8	2b	-G-G-G-A-C-CG-A-T-C---G-G-T---A-T-	
PC1_37	5a	-G---TG---G-CC---G-C-C-T-A-GGTG-T-CG-A-	
PC1_48	5a	-G---TG---G-CC---G-C-C-T-A-GGTG-T-CG-A-	
BR36	3a	-A-G---C-G-CC-A-G-C-C-T---GTC-T-T-T-	

Figure 10 - Continued 8

		5041		5090																													
HCV-1	1a	GT	CAT	AGTGGCAGGGTCTTGTCTCCGGGAAGCCGGCAATCATACTGA																													
HCV-J	1b	---	T	---	A	---	A	---	G	---	A	---	TG	T	---	C	---																
HC-J6	2a	TG	---	CA	---	C	---	CT	---	GCA	---	G	---	TAA	---	CA	---	CGAG	---	C	---	TGC	---	TGC	---	---							
HC-J8	2b	TC	---	CA	---	T	---	C	---	CC	---	ACA	---	C	---	AAT	---	ATCG	---	GT	---	TTG	---	GGCC	---	C	---						
PC1_37	5a	C	---	---	C	---	T	---	A	---	A	---	C	---	C	---	T	---	A	---	T	---	C	---	---	---							
PC1_48	5a	---	---	C	---	T	---	A	---	A	---	C	---	C	---	T	---	A	---	T	---	C	---	---	---	T	---	C	---				
BR36	3a	---	G	---	T	---	---	TC	---	ATA	---	---	AGC	---	GGG	---	C	---	---	---	G	---	T	---	---	---	A	---					
		5091		5140																													
HCV-1	1a	CAG	GG	AAGTCTCTACCGAGAGTTCGATGAGATGGAAGAGTGTCTCAGC																													
HCV-J	1b	---	---	---	---	AG	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
HC-J6	2a	---	A	---	G	---	---	TG	---	AG	---	CT	---	T	---	---	---	G	---	A	---	TG	---	CT	---	CTA	---	---	---	---	---		
HC-J8	2b	---	A	---	A	---	T	A	---	TG	---	AG	---	CC	---	T	---	---	---	A	---	G	---	CT	---	CCA	---	---	---	---	---		
PC1_37	5a	T	---	G	---	AT	---	A	---	AGC	---	A	---	T	---	---	---	G	---	---	---	---	---	---	---	---	---	---	---	---	---		
PC1_48	5a	T	---	G	---	CAT	---	A	---	AGC	---	A	---	T	---	---	---	G	---	---	---	---	---	---	---	---	---	---	---	---	---		
BR36	3a	---	AA	---	G	---	GT	---	G	---	T	---	A	---	C	---	A	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
		5141		5190																													
HCV-1	1a	ACT	TACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAG																														
HCV-J	1b	---	C	---	C	---	T	---	---	---	A	---	---	---	CA	---	---	---	A	---	---	---	---	---	---	---	---	---	---	---	---		
HC-J6	2a	GAG	CGG	---	TCT	---	T	---	AG	---	G	---	CA	---	CG	---	A	---	A	---	---	---	AT	---	C	---	G	---	---	---	---	---	
HC-J8	2b	---	AG	---	CGG	---	CCT	---	T	---	G	---	---	---	CA	---	CG	---	A	---	G	---	---	AT	---	C	---	---	---	---	---	---	
PC1_37	5a	CG	---	G	---	C	---	T	---	G	---	CG	---	AC	---	ACGT	---	GCCA	---	T	---	GA	---	A	---	---	---	---	---	---	---	---	
PC1_48	5a	CG	---	G	---	C	---	T	---	G	---	CG	---	GAC	---	ACGT	---	GCCA	---	T	---	GA	---	A	---	---	---	---	---	---	---	---	
BR36	3a	CT	GC	---	A	---	---	---	A	---	T	---	---	---	A	---	---	---	CT	---	CA	---	G	---	AA	---	A	---	---	TC	---	---	---

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Figure 10 - Continued 9

		5191		5240
HCV-1	1a	AAGCCCTCGCCTCCTGCAGACCGCGTCCCGTCAGGCAGAGTTATCGC		
HCV-J	1b	-----G-----AT-G-----A-A-CA-AAG-A-G-----C-GCT--		
HC-J6	2a	---AT-AA---T-AT-----CAA-T---AAA-A-TC-A-AC--ACA		
HC-J8	2b	---ATA-AA-----A-ACAG--CA-AA-G-A-TC-A-AC--ACA		
PC1_37	5a	--A-TG-----T-A-CAGC-GA-CGG--AGA---T--AAC-C-GAA		
PC1_48	5a	--A-TG-----T-A-CAGC-GA-CGG--AGA---T--AAC-C-GAA		
BR36	3a	--A-T---T-AT-G-----CGA-CA--AA-ACA-CT--C--T-A		
		5241		5290
HCV-1	1a	CCCTGCTGTCAGACCAACTGGCAAAACTCGAGACCTTCTGGGCGAAGC		
HCV-J	1b	T--C-TG--GG--T-----G---G-GCC--T---GT-----A-		
HC-J6	2a	A-C-----G--G-TTCT-----CC-GG-A-CAA-----C-A-		
HC-J8	2b	G-A--A-A--T-ATCA--CC-G-T-ACAA-T-----C-A-		
PC1_37	5a	G-G-A-C-AC-T-TGTG--A-C-GGCT--CAG-----N-C-CAT		
PC1_48	5a	G-G-A-C-AC-T-TGTG--A-C-GGCT--CAG-----N-C-CAT		
BR36	3a	G--CATA-AACT-----G-T--G---T--CAC----		
		5291		
HCV-1	1a	AT		
HCV-J	1b	-C		
HC-J6	2a	-C		
HC-J8	2b	-C		
PC1_37	5a	-C		
PC1_48	5a	-C		
BR36	3a	--		

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SEQ ID NO

Figure 11

	1286	
HCV-1	TTGSPITYTYGKFLADGCGSGGAYDIIICDECHSTDATSILGIGTVLDQAEAGARIVV	
HCV-J	---G---C---S-T---	
HC-J6	---A---A---AV-S-T---	V-T-
HC-J8	---DS---I---AA---V-T---	V-
PC-1-48	---AS---V---Q-T---	
PC-1-37	---AS---H-V---Q-T---	
		56
		58
	1346	
HCV-1	LATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIKGRHLIFCHSKKKCDELAA	
HCV-J	---I---N---I-A---	
HC-J6	---T---GQE---R---SY---	
HC-J8	---T-T-S---GHE---AF---	
PC-1-48	-X-X-T---PQE-V-XR-AF---	
PC-1-37	---X---T---PQE-V-R-AF---N---	

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Figure 11 - Continued 1

	1406	KLVALGINAVYRGLDVSPIPTSGDVVVVAIDALMTGYTGDFDSVIDCNCVCVTQTVDIFS
HCV-1		--TG--L--
HCV-J		--F--
HC-J6		A-RGM-L--
HC-J8		--Q--
		--F--
		--VA--V--
		--VA-S-I--
	1466	LDPTFTIETITLPQDAVSRTQRRGRTGRGKPGIYRFVAPGERPSGMFDSSVLCCEYDAGC
HCV-1		--T--
HCV-J		--A--
HC-J6		--RS--
HC-J8		--T--
		--T-Q-V--
		--S--
		--RL-V-Y-SS--
		--V--
		--A--
	1526	AWYELTPAETTVRLRAYMNTPLPVCQDHLFEWEGVFTGLTHIDAHLFSLQTKQSGENLPY
HCV-1		--S--
HCV-J		--L--
HC-J6		--F--
HC-J8		--A--
		--A--
		--G--
		--FA--

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Figure 11 - Continued 2

1586	
HCV-1	LWAYQATVCARAQAPPPSDQMWKCLIRLKP TLHGPTLLYRLGAVQNEITLTHPVTKYI
HCV-J	-----I-----
HC-J6	-T-----K-----V-----T-----V-----S-T-V-----
HC-J8	-T-----K-----V-----T-----T-----T-V-----
1646	
HCV-1	MTCMSADLEVVTTWVLVGGVLAALAAAYCLSTGCWVIVGRVVLSGKPAIIPDREVLYREF
HCV-J	-A-----T-S-----II--R-V-----Q-----
HC-J6	A--Q-----M-----A-----V-----A--C-I--LHVNRVVA--K--EA--
HC-J8	A--Q-----IM--S--A-----V-----A--IS-I--LH-NDRVVA--K-I--EA--
PC-1-48	-A-----I-X-----V-X-----TV-S-A--II-----A-XQ--
PC-1-37	-AF-P-----I-X-----V-T-XX--TV-S-A--II-----X--QQ--
1706	
HCV-1	DEMEECSQLHPYIEQGMMLAEQFKQKALGLLOTASRQAEVIAPAVOTNWOKLETFWAKH
HCV-J	-----AS-----Q-----TK--AA--V-ESK-RA--V-----
HC-J6	-----ASRAAL--E-ORI--ML-S-IQ-----Q--K-QD-Q--AS-P-V-Q-----
HC-J8	-----ASKAAL--E-QRM--ML-S-IQ-----Q-T--QD-Q--I-SS-P--Q-----
PC-1-48	-----AS--MDETRAI-G--E-V--FIS-TGQK--TLK--ATSV-N-AXQ--TY
PC-1-37	-----AS--MDETRXI-G--E-V--FIS-TGQK--TLK--ATSV-N-ADQ--XTY

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Figure 12 - Continued 1

	430	440	450	460	470	
	-*		*	-		*
1a	NCNDSLNTGWL	AGLFYHHKFNSSG	CPERLASCRPLTD	FDGNGPISY	AN	
HCV1						
1b	-----Q--FI--A--	A--R--A--	M-----	IDE--A--	TH DM	
HCJ6	-----H--F--S--	T--S-----	MSA--SIEA--RV--	ALQ--ED--		
2a	-----Q--F--S--	T-----	S--G--D--RI--	TLE--ET--		
HCJ8	-----E--I--	FI-----Y-----	T-----Q--S--K--I--F--R--	LTD --		
NZL1						
3a						
3b						
HCVTR						
BE95	-----Q--FI--	Y-----D--M--	A--AT--	T--		
	480	490	500	510	520	
1a	GSGP/DORPYCMHYPPKPCGIVPAKSVCGPVYCF	TPSPVWVGT	TDRSGAP			
HCV1						
1b	PESS/-----	A--R-----	SQ-----	F-----		
HCJ6	VTN--E--M--	RQ--V--S--S--	L-----			
2a	VTNDG--M--	R-----RT-----	KQ--V--			
HCJ8	IT--S--D--	A--R--D--S--				
NZL1						
3a						
3b						
HCVTR						
BE95	I--S--DK--	R--V--QE--	SK--H--			

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Figure 12 - Continued 2

		530	540
			*
		TYSWGEN	TDVFLN
		-----	E---LL--TRP-QG
		--T-----	E---L--S----
		--T-----	E---L--S----
		--N--S-V--	F-LM-----I
HCV1	1a		
HCVJ	1b		
HCJ6	2a		
HCJ8	2b		
NZL1	3a		
HCVTR	3b		
BE95	5a		

Figure 13

	SEQ ID		980
HCV-1	1a	CCCTACGACGGCGTTGGTAATGGCTCAGCTGCTCGGATCCACAAGCC	
HCH-H	1a	-----G-A-----GG-A-----A-----	
HC-J1	1a	-----G-----	
HCV-J	1b	-A-----A-----CC-A-GG-AT-G-----A-----	
HCV-BK	1b	-G-C-A-A-CC-A-GG-T-G-T-A-----	
HC-J4.83	1b	-A-----A-A-CC-A-GG-T-G-T-----T-----	
HC-J4.91	1b	-A-----A-A-CC-A-GG-T-G-T-----T-----	
HCV-JTA	1b	-G-----A-A-CC-A-GG-T-G-T-A-----T-----	
HCV-JTB	1b	-G-----A-A-CC-A-GG-T-G-T-A-----T-----	
HCV-CHINA	1b	-G-----A-A-TC-A-GG-T-G-T-A-----T-----	
HCV-T	1b	-G-----A-C-A-GG-T-G-T-----T-----	
HCV-JK1	1b	-A-----A-A-C-A-GG-T-G-T-A-----	
HCUNK	1b	-G-----A-A-CC-A-GG-AT-G-----A-----T-----	
HCV-N	1b	-A-----A-A-CC-C-G-T-G-T-A-----	
HC-J6	2a	-G-C--G-TA-CA-A-CC--GT-CGC-A-G-CG--CG-G-T-	
HC-J8	2b	-T-A--TCTTA-CA-A-CC-C--CT-CGCCGT--TG-T-CG--CTG	
HC-J5	2a	-A-C--G-CA-CA-A-CC--GT-CGC-A-G-CG--CG-G-TT	
HC-J7	2b	-A-A--TCTTA-CA-A-CC-C--CT-TGCCGT--TG-T--TG-GCTA	
NZL1	3a	---CG-TGT--GTA---GG---G--TG-C-G--TT-A-C-GA--	
HEM26	3a	---CG-TGT--GTA---GG---G--CG-C-G--TT-G-C-GA--	
TH85	3a	---CG-CGT--GTA---GG-A--G--TG-C-G--TT-G-C-GA--	
US114	3a	---CG-CGT--GTA---GG---G--CG-T-G--TC-G-C-GA--	
BE95	5a	-A-----A--TC--C-GG---C--T-A-G-----T-C-----TG	

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Figure 13 - Continued 1

		1030	
		ATCTTGGACATGATCGTGGTGCTCACTGGGGAGTCCTGGCGGGCATAGC	
		---A---C-C----AA	
		---T---T---A-	
		G-G-G-G-G-G-T- A- C-T-	
		G-G-G-G-G-G-C- C-T-	
		G-G-G-G-G-G-C- C-T-	
		G-G-G-G-G-G-C- C-T-	
		G-G-G-G-G-G-C- A- C-T-	
		G-G-G-G-G-G-C- A- C-T-	
		G-A-G-TG-G-C- C-T-	
		G-G-G-G-G-G-C- C-T-	
		G-G-G-G-G-G-C- C-C-	
		G-G-G-G-G-G-C- A- C-T-	
		G-A-C-G-G-G-C- C-T-	
		---A-A---C-T-GC-G- T- C-A-TTC-T-	
		G-C-C-A-T-TTTC-C-GC-T- T-GG-TTT-T-G-	
		---A-A---C-TAGC-G- C-A-TTC-C-	
		G-C-T-GG-TG-TTC-C-GC-T- C-GG-TTT-T-G-	
		T-G-C-A-G-C-G-C-T- CA-T- C-G-	
		T-G-C-A-A-C-G-C-T- CA-T- C-	
		T-G-C-A-A-C-G-C-T- CA-T- C-	
		T-G-C-T-AG-A-C-G-C-T- CA-T- C-	
		G-A-T-C---A-GAGC- G-T-TTT-C-GCC-	
HCV-1	1a		
HCH-H	1a		
HC-J1	1a		
HCV-J	1b		
HCV-BK	1b		
HC-J4.83	1b		
HC-J4.91	1b		
HCV-JTA	1b		
HCV-JTB	1b		
HCV-CHINA	1b		
HCV-T	1b		
HCV-JK1	1b		
HCUNK	1b		
HCV-N	1b		
HC-J6	2a		
HC-J8	2b		
HC-J5	2a		
HC-J7	2b		
NZL1	3a		
HEM26	3a		
TH85	3a		
US114	3a		
BE95	5a		

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Figure 13 - Continued 2

	1080		GTATTCTCCATGCTGGGAACTGGCGAAGTCTCTGGTAGTCTGCTGCG
			-----T-----
HCV-1	1a		C-C-AT-----T-A-T-A-----A
HCH-H	1a		C-C-AT-----C-----T-A-T-A-----A
HC-J1	1a		C-C-AT-----A-----T-A-T-GC-----A
HCV-BK	1b		C-C-AT-----A-----T-A-T-GC-----A
HC-J4.83	1b		C-C-AT-----T-----T-A-T-A-----A
HC-J4.91	1b		C-C-AT-----T-----T-A-T-A-----A
HCV-JTA	1b		C-C-AT-----T-----T-A-T-A-----A
HCV-JTB	1b		C-C-ATG-----T-----T-A-T-A-----A
HCV-CHINA	1b		C-C-AT-----T-----T-AA-T-A-----A
HCV-T	1b		C-C-AT-----T-----T-A-T-A-----A
HCV-JK1	1b		C-C-AT-----T-----T-AA-T-C-A-----A
HCUNK	1b		C-C-AT-----C-----T-A-T-A-----A
HCV-N	1b		C-C-----T-CA-AGCG-----A-A-G-T-CA-T-TT-----
HC-J6	2a		C-----CAA-AGCG-----C-A-A-C-CCA-C-C-T-----
HC-J8	2b		C-C-----T-CA-AGCG-----G-T-CA-C-T-----
HC-J5	2a		C-----CA-AGCG-----C-A-A-T-CCA-C-C-C-----
HC-J7	2b		C-----CA-----C-----GCAA-CA-CA-G-TA-----
NZL1	3a		C-A-----CA-C-T-----C-----GCTA-CA-CG-G-TA-----
HEM26	3a		C-----CAA-C-----C-----GCTA-CA-CA-G-TA-----
TH85	3a		C-----CA-----C-----GCTA-CA-CA-G-TA-----
US114	3a		A-C-ATG-ATC-----CT-----A-C-----G-C-G-CT-T-T-----
BE95	5a		

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Figure 13 - Continued 3

1130	TATTTGCCGGCGT	CGACGGGAAAC	CCACGTCACCGGGGAAGTGCCGGC
HCV-1	1a	-G-----T-----T-----AT-----T-----CAA-----C-	-G-----T-----T-----G-C-C-----G-A-----G-TA-C-
HCH-H	1a	-C-----T-----T-----G-T-----G-A-----GGCGCAA-C-	-C-----T-----T-----G-G-----T-ACGT-G-----GGCG--A-
HC-J1	1b	-C-C-----T-----T-----G-CG-----T-ACGT-G-----GGTG-----	-C-----T-----T-----G-T-C-----TT-ACG-A-----GTCGCAA-CT
HCV-BK	1b	-C-----T-----T-----T-G-T-----T-OGT-T-----GTCGCAA-CT	-T-----T-----T-----G-AGT--AT--GT-A-A--G-CA-TG-C-
HC-J4.83	1b	-C-C-----T-----T-----T-G-AGT--AT--GT-A-T-----GCA--AA-	-T-----T-----T-----GAACC-----G-A-----GGCGCAA--T
HC-J4.91	1b	-T-----T-----T-----G-C-C-----T-ACA-G-----GCAC--T-C	-GGCC-----G-G-----C-----TAC-GTT-----TTC-A--CG
HCV-JTA	1b	-TG-----G-A-G-T-AACC--T-TTC-G--CGAGAA--G--T	-GGCC--T-A-G-T-A-C-----G-AC-GTT-C--TTC--T-CG
HCV-JTB	1b	-TG-C--A-A-G-T-AGC-----A--T--C--CAA--G-C	-G-CT-A-G-----T-CC-C-AT-TAC-----T-C-C--ATCT
HCV-CHINA	1b	-G--T-A-G-----T-C--AT-TAC-----T-C--TG-CT	-G--T-A-G-----T-C-G-A-G-A-----T-C-C--A-CT
HCV-T	1b	-G--T-A-G-----T-CAGC--A--TA-----T-CTC-ATG-CT	-G-----A-G-T-T-TACT-----GA-TT-G-C--CTCCAG--C-
HCV-T	1b		
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HCV-T	1b		
HCV-T	1b		</

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Figure 13 - Continued 4

		1180
HCV-1	1a	CACACTGTGTCTGGATTGTTAGCCTCTCTCGCACCGGCCAAGCAGAA
HCH-H	1a	-G---CAC-G---GC---G-T---TA-----
HC-J1	1a	-G-G-CA-----C-----T-T-A-----T-----
HCV-J	1b	TC--GCACCCAGA-CC-C-GTC-TGG--T--A---C-ATCT--
HCV-BK	1b	A-A-CACCAACA-GC-C-GTC-A-GT---AGT-GC-GTCT--
HC-J4.83	1b	-----CACC--CACGC-C-CGTC--T-T---T-G-GTCT--
HC-J4.91	1b	-G---CACC--C-G-C-CACGTC--T-T-T-T-G-GTCT--
HCV-JTA	1b	-G-CACACCCAGA-CG-CACGTC-T-T-A-C-A--GC-GGCC--
HCV-JTB	1b	-G-CACACCCAG--GG-C-CGTC-T-T-A-C---GC-GGCC--
HCV-CHINA	1b	-G-T-CACCCTC--G-CACGTC--T-TA---T-G-TCT--
HCV-T	1b	-G---CACCCACA-TC-C-CGTCT--T-TA--A--G-GTCC--
HCV-JK1	1b	-G-CACCCGGC-CG--CGTC-T-T-AGT-T--T-GGCT--
HCUNK	1b	-GGG-C-CTAGCTCGC-AACGTC--T-TAGC-T--GC-GGTT--C-
HCV-N	1b	---CTCACCAGC--G--C-CGG---T-TA--T--GC-GTCT--G
HC-J6	2a	--T-AC-CCAGACCC-CACCG--A-GT--T-C-TT--T--G--
HC-J8	2b	-GT--C-CG-G-G--C-C-G---T-TA-TA-T-T-----
HC-J5	2a	GCA--CACCAGG--C-CACC--A-GT--T-CT-T--T-G-----
HC-J7	2b	--T--C--TAGA--G-C-CC--A--T-AGC--T--T-CG-----G-
NZL1	3a	-GTCA-ACCCAA-CG---C-G-T--TT-T-ACAT--C-C-A--
HEM26	3a	--TG--ACCAGA--GA-A-C--T--TT-TA-TGTG-----CGC--
TH85	3a	--TGA--C-ACA-G--C---TT--AAT-GG-----CGA--A-
US114	3a	-GTGA--C-C-ACA-G--CAC-G--T-TT---C-GG--C--GT--
BE95	5a	--A--GAC--A---CA-C-CCTCAT-TA--A-C-GC-----GC--

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Figure 13 - Continued 5

	1230	
HCV-1	1a	CGTCCAGTGTATCAACACCAACGGCAGTTGGCACCTCAATAGCACGGCCC
HCH-H	1a	-A-----A-----A-----A-----A-----T
HC-J1	1a	-A-----A-----A-----A-----A-----T
HCV-J	1b	AA---A---CG-G-----C-----A-----A-----C-G-C-T
HCV-BK	1b	AA---T-A-----T-G-----A-----A-----C-G-T
HC-J4.83	1b	AA---TG-G-T-----C-----A-----C-G-T
HC-J4.91	1b	AA---TG-G-T-----C-----A-----C-G-T
HCV-JTA	1b	AA---C-A-----T-----C-----A-----C-G-T
HCV-JTB	1b	AA---C-A-----T-----C-----A-----C-G-T
HCV-CHINA	1b	GA---T-A-T-----T-T-C-----TA-----C-G-T
HCV-T	1b	AA---T-A-----T-----C-----A-----C-G-T
HCV-JK1	1b	AA---A-TG-T-----T-----A-----C-G-T
HCUNK	1b	-C-----C-A-----C-----TA-----C-G-C
HCV-N	1b	AA---T-A-----T-----A-----C-G-T
HC-J6	2a	AA---C-----T-----A-----A-----C
HC-J8	2b	-C-T-TT-A-----T-----C-----A-A-CC-G-T
HC-J5	2a	-C-T-----C-T-----T-C-----A-CC-T
HC-J7	2b	TA-AGT-A-----T-----C-----A-A-CC-G-C
NZL1	3a	AC-G-----G-----T-----TCG-----A-----C-T-T
HEM26	3a	AC-G-----G-----T-----TCG-----A-----C-T-T
TH95	3a	-C-G-T-G-----T-----TCG-----A-----A-T
US114	3a	-C-G-----G-----T-----TCG-----TA-----CC-T
BE95	5a	AC-G-----C-A-T-----A-C-----A-----C-G-C

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Figure 13 - Continued 6

	1280	
	TGAACTGCAATGATAGCTCAACACCGGCTGGTTGGCAGGGCTTTTCTAT	
HCV-1	1a	-----A-----T-----A-----C-----
HCH-H	1a	-----A-----T-----A-----A-----
HC-J1	1a	-----A-----T-----A-----A-----
HCV-J	1b	-----CTC-----C-A-T-G-TCA-T-T-C-G-----A-----
HCV-BK	1b	-----CTCT-----C-G-T-G-TTC-T-T-C-G-----C-----
HC-J4.83	1b	-----A-----CTC-----C-----T-G-TCC-T-C-C-G-----C-----
HC-J4.91	1b	-----A-----T-----CTC-----C-----T-G-TCC-T-C-C-G-----C-----
HCV-JTA	1b	-----ATC-----G-TC-T-T-C-CA-G-----C-----
HCV-JTB	1b	-----ATC-----G-TC-T-T-C-CA-G-----C-----
HCV-CHINA	1b	-----CTC-----T-T-G-TTC-T-T-C-G-----C-----
HCV-T	1b	-----A-----C-CTC-----C-G-T-G-TTC-T-T-C-G-----C-----
HCV-JK1	1b	-----T-----C-GTC-A-----T-G-TC-T-T-C-C-G-----C-----
HCUNK	1b	-----G-----CTC-----T-G-TTG-T-T-C-C-G-----C-----
HCV-N	1b	-----CTC-----C-G-T-G-TCC-T-T-C-C-G-----C-----
HC-J6	2a	-----CTCTT-GC-----TCC-C-GTCA-G-----C-----
HC-J8	2b	-----C-----T-AC-G-G-T-TCC-C-TTCCT-G-T-C-----C-----
HC-J5	2a	-----T-----CTC-T-G-----TTA-C-GTCC-G-----C-----
HC-J7	2b	-----C-----T-GC-A-A-T-TC-C-T-CC-G-T-C-----C-----
NZL1	3a	-----A-----GTC-A-A-----G-TTA-A-T-T-G-T-----C-----
HEM26	3a	-----GTC-A-A-----G-TCA-A-T-T-A-T-----C-----
TH85	3a	-----TC-A-A-----G-TCA-A-TA-T-G-T-----C-----
US114	3a	-----GTC-A-A-----G-TCA-A-T-T-GC-T-----C-----
BE95	5a	-----T-T-T-----C-----C-G-T-T-G-TCA-A-C-C-C-----C-----

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Figure 13 - Continued 7

		1330
HCV-1	1a	CACCACAAGTTCAACTCTTCAGGCTGTCTGAGAGGCTAGCCAGCTGCCG
HCH-H	1a	-G---A---T-G---
HC-J1	1a	--A---A---G---C---T-G---
HCV-J	1b	GCA---G---G-G-C-G-C-A---C-CA-G-T---
HCV-BK	1b	ACA-T-GT---G-C-G-C-A---C-CA-G-T---
HC-J4.83	1b	ACA---G---G-C-G-C-G---C-CA-G---
HC-J4.91	1b	ACA---G---G-C-G-C-G---C-CA-G---
HCV-JTA	1b	GCA---G---G-C-A-C-A---C-CA-G---
HCV-JTB	1b	GCA---G---G-C-A-C-A---C-CA-G---
HCV-CHINA	1b	ACA---G---G-G-C-A-CG-A---C-CA-G---
HCV-T	1b	GCG---G---G-G-C-G-C-A---C-CA-G---
HCV-JK1	1b	GTAAG---G---G-T-A-CT-A---C-CA-G-T---
HCUNK	1b	A-AT---G---G-G-C-G-C---C-CT-G---CG---
HCV-N	1b	ACAT---G---G-C-A-C-G-G-C-CA-G---
HC-J6	2a	AC---GC---G---A---C---AC-CA-GT-GC---
HC-J8	2b	AC---AGC-T---C---C---C-CT-GT-TTC---
HC-J5	2a	GT-A-CGC---T-G---A---CC-TC-C-GT-GT---
HC-J7	2b	GT-AGACGT---AGC-T---C---C---C-CT-GT-TTC---
NZL1	3a	T---T---A-T-A---C-A---CAG---AA---
HEM26	3a	T-T-T---A-T-A---C-C---CAG---TAA---
TH85	3a	T---T---A-T-A---C-A---CAG---AA---
US114	3a	T-TA-T---A-T-A---C-A---CAG-T---AA---
BE95	5a	T---T---T-A-A-C-G-G-TC-A-G-T---TA---

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Figure 13 - Continued 8

HCV-1	1a	1380	ACCCCTTACCGATTTTGTACAGGGCTGGGCCCTATCATGTTAT	GCCTA
HCH-H	1a		--G-----C-----T-----	----
HCV-J	1a		--G-----C-----T-----	----
HCV-J1	1b		C---A-CGAT--G-C-CT--G-----T-C---C-C-	--AT-
HCV-BK	1b		CA--A--GA-A-G-C-----A-----T-C-T-C-	--TG
HC-J4.83	1b		C---A--GA-TGG-C-C-----A-----C---CC-	A-TG
HC-J4.91	1b		C---A--GA-GG-C-C-----A-----C---CC-	A-TG
HCV-JTA	1b		CT--A--CGA-A-G-C-CT--A-----C---CC-	A-G
HCV-JTB	1b		CT--A--GA-A-G-C-CT--A-----T-C---CC-	A-G
HCV-CHINA	1b		C---A--GATACA-C-T-----C-----C---C-	A-TG
HCV-T	1b		TT--A--GA-A-G-C-T-----A-----T-C---CC-	A-TG
HCV-JK1	1b		T---A--GA-AGG-C-CT--A-G-----T-C---CCC-	--TG
HCUNK	1b		C---A--GAVACA-C-CG-----G-----T-C---C-C	A-TG
HCV-N	1b		CT--A--GA-A-G-C-----A-----T-C---C-	--TG
HC-J6	2a		CAGTA-CGAG-CC---CGGGT--A-----G-CT-ACAA--GAG-A--	
HC-J8	2b		CGGG--GGA-----CG-ATC-----AA-CT-GGAA--CGAA--	
HC-J5	2a		CAG-A-CGAG-C---CCGATA-G-----A-CT-GCAA--CGAG-AT-	
HC-J7	2b		TAAG--GGAT-----CG-ATC-G-----AA-CT-GGAA--GAGA--	
NZL1	3a		G---A-C-TTTC-CAGG-----A-----CT-A-CAG--	--T-
HEM26	3a		G---A-C-TTCC-CAGG-----G-----T-CT-G-CAG--	--T-
TH85	3a		G---A-C-TCC-CA-T-----G-----CT-G-CAG--	--AA-
US114	3a		G---A-C-TTCC-CAGG-----G-----T-CT-G-CAG--	--T-
BE95	5a		GG-----G-AC-----AA-----C-----	----

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Figure 13 - Continued 9

	1430	
HCV-1	ACGGAAGCGGCCCC	GACCAGGCCCCCTACTGTCTGGCACTACCCCCCA
HCH-H	-----T-	--G-A-----T--
HC-J1	-----T-	--A-----T-T--
HCV-J	TGCCTGAGA-T-G	-----A-G-A-T-----G-G-T
HCV-BK	-GTCT--A-AT-A	-----A-G-A-T-----A-T
HC-J4.83	-GCCTGA-A--G	-T--A-G-T-T-----T--G-G-T
HC-J4.91	-GCCT-A-A--G	-T--A-G-T-T-----T--G-G-T
HCV-JTA	-GCCT-G-A-TG	-T--A-G-T-----T--G-A-T
HCV-JTB	-GCCTG-G-A-TTG	-T--A-G-T-----T--G-A-T
HCV-CHINA	-GCCTGATA-T-G	-----A-G-T-T-----G-G-T
HCV-T	-G-CTGA-AT-AG	-----A-G-T-T-----G-A-C
HCV-JK1	-GTCTC-A-T-G	-----AA-G-T-----G-A-T
HCUNK	-GCCTCAT-ATTG	-T--A-G-----T-----G-G-T
HCV-N	-TCCT-AA-A--G	-----A-G-T-T-----G-A--
HC-J6	-T-TC-C-AAT--AGAG-	TAT-A-A-G-T-----A--
HC-J8	-TC-C-AA-GATGGG-	-AT-A-G-G-----T-----G
HC-J5	-T-TC-C-AAT--AGAA-	TAT-A-A-A-T-----A--
HC-J7	-T-TC-C-AA-GAGGAG-	-AT-A-A-G-----T--T-G
NZL1	-ATC-C--T--TTCT-	TG-CA-A-A-----T--G-A-T
HEM26	-ATCTC--TT-GTCC-	AG-CAAA-G-----G-A-T
TH85	-ATC-C--T--TCT-	TG-CAAA-A-----G-A-T
US114	-ATC-C-ATT-TTCT-	TG-CAAA-G-----G-A-T
BE95	--AT-TCG--T--AGT-	TG-CAAA-A-T-----T--

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Figure 13 - Continued 10

HCV-1	1a	1480	AAACCTTGGGTATTGTGCCCGAAGAGTGTG
HCH-H	1a		-G-----T-C-----A-----C--
HC-J1	1b		-----C-----A-----C-A
HCV-J	1b		CG--G--G--C--T--TC-CAG--
HCV-BK	1b		CC-AA-TACC-C-A-T--TC-GAG--
HC-J4.83	1b		CG--G--T--C-A--TC-CAG--
HC-J4.91	1b		CG--G--T--C-A--TC-CAG--
HCV-JTA	1b		CGG-AG-T--C-A-T--TC-CAG--
HCV-JTB	1b		CGG-AG-T--C-A--TC-CAG--
HCV-CHINA	1b		CG-AAG--C-C-A-T--TC-GAG--
HCV-T	1b		CGG-G-T--C-A--TC-CAG--
HCV-JK1	1b		C--G-T--C--TT-CAG--
HCUNK	1b		C--G-T--A--TT-CAG--
HCV-N	1b		C--AG-T--CA-A--CG-TCCGAG-C-
HC-J6	2a		-G-AG-T--G-A-CT--GCTC--
HC-J8	2b		-GG--C-C-C-G-T-G-CG-T
HC-J5	2a		---G-T-C-A-C--G-TC--
HC-J7	2b		-G--C-C-CT-G-T--CG-C
NZL1	3a		-G--T-AC--C-G-ATCA--C
HEM26	3a		-G--TACCG--C-A-ATCA--C
TH85	3a		-G--TAAA-G--C-A-ATCA--C
US114	3a		-G-T--T-A-CC-C-G-ATCA--C
BE95	5a		CGG-G--AG-G--A--CC-AGAG--C